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(57) Abstract

Novel nucleic acid sequences isolated from *Photorhabdus luminescens*, whose expression results in novel insecticidal toxins, are disclosed herein. The invention also discloses compositions and formulations containing the insecticidal toxins that are capable of controlling insect pests. The invention is further drawn to methods of making the toxins and to methods of using the nucleotide sequences, for example in microorganisms to control insect pests or in transgenic plants to confer insect resistance.

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INSECTICIDAL TOXINS FROM PHOTORHABDUS

The invention relates to novel toxins from *Photorhabdus luminescens*, nucleic acid sequences whose expression results in said toxins, and methods of making and methods of using the toxins and corresponding nucleic acid sequences to control insects.

Insect pests are a major cause of crop losses. Solely in the US, about $7.7 billion are lost every year due to infestation by various genera of insects. In addition to losses in field crops, insect pests are also a burden to vegetable and fruit growers, to producers of ornamental flowers, and they are a nuisance to gardeners and home owners.

Insect pests are mainly controlled by intensive applications of chemical insecticides, which are active through inhibition of insect growth, prevention of insect feeding or reproduction, or death of the insects. Good insect control can thus be reached, but these chemicals can sometimes also affect other, beneficial insects. Another problem resulting from the wide use of chemical pesticides is the appearance of resistant insect varieties. This has been partially alleviated by various resistance management strategies, but there is an increasing need for alternative pest control agents. Biological insect control agents, such as *Bacillus thuringiensis* strains expressing insecticidal toxins like d-endotoxins, have also been applied with satisfactory results, offering an alternative or a complement to chemical insecticides. Recently, the genes coding for some of these d-endotoxins have been isolated and their expression in heterologous hosts have been shown to provide another tool for the control of economically important insect pests. In particular, the expression of insecticidal toxins in transgenic plants, such as *Bacillus thuringiensis* d-endotoxins, has provided efficient protection against selected insect pests, and transgenic plants expressing such toxins have been commercialized, allowing farmers to reduce applications of chemical insect control agents. Yet, even in this case, the development of resistance remains a possibility and only a few specific insect pests are controllable. Consequently, there remains a long-felt but unfulfilled need to discover new and effective insect control agents that provide an economic benefit to farmers and that are environmentally acceptable.

The present invention addresses the need for novel insect control agents. Particularly needed are control agents that are targeted to economically important insect pests and that efficiently control insect strains resistant to existing insect control agents.

Furthermore, agents whose application minimizes the burden on the environment are desirable.

In the search of novel insect control agents, certain classes of nematodes from the genera *Heterorhabdus* and *Steinernema* are of particular interest because of their insecticidal properties. They kill insect larvae and their offspring feed in the dead larvae. Indeed, the insecticidal activity is due to symbiotic bacteria living in the nematodes. These symbiotic bacteria are *Photorhabdus* in the case of *Heterorhabdus* and *Xenorhabdus* in the case of *Steinernema*.

The present invention is drawn to nucleic acid sequences isolated from *Photorhabdus luminescens,* and sequences substantially similar thereto, whose expression results in toxins that are highly toxic to economically important insect pests, particularly insect pests that infest plants. The invention is further drawn to the toxins resulting from the expression of the nucleic acid sequences, and to compositions and formulations containing the toxins, which are capable of inhibiting the ability of insect pests to survive, grow or reproduce, or of limiting insect-related damage or loss in crop plants. The invention is further drawn to a method of making the toxins and to methods of using the nucleic acid sequences, for example in microorganisms to control insects or in transgenic plants to confer insect resistance, and to a method of using the toxins, and compositions and formulations comprising the toxins, for example applying the toxins or compositions or formulations to insect-infested areas, or to prophylactically treat insect-susceptible areas or plants to confer protection or resistance to the insects.

The novel toxins are highly active against insects. For example, a number of economically important insect pests, such as the Lepidopterans *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Manduca sexta* (Tobacco Hornworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), as well as the Coleopterans *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle) can be controlled by one or more of the toxins. The toxins can be used in multiple insect control strategies, resulting in maximal efficiency with minimal impact on the environment.

According to one aspect, the present invention provides an isolated nucleic acid molecule comprising: (a) a nucleotide sequence substantially similar to a nucleotide

sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11; (b) a nucleotide sequence comprising nucleotides 23,768-31,336 of SEQ ID NO:11; or (c) a nucleotide sequence isocoding with the nucleotide sequence of (a) or (b); wherein expression of the nucleic acid molecule results in at least one toxin that is active against insects.

In one embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1. Preferably, the nucleotide sequence is substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1. More preferably, the nucleotide sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs:2-6. Most preferably, the nucleotide sequence comprises nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

In another embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 15,171-18,035 of SEQ ID NO:11. Preferably, the nucleotide sequence is substantially similar to nucleotides 15,171-18,035 of SEQ ID NO:11. More preferably, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:12. Most preferably, the nucleotide sequence comprises nucleotides 15,171-18,035 of SEQ ID NO:11.

In still another embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 31,393-35,838 of SEQ ID NO:11. Preferably, the nucleotide sequence is substantially similar to nucleotides 31,393-35,838 of SEQ ID NO:11. More preferably, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:14. Most preferably, the nucleotide sequence comprises nucleotides 31,393-35,838 of SEQ ID NO:11.

In yet another embodiment of this aspect, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:13, and preferably comprises nucleotides 23,768-31,336 of SEQ ID NO:11.

In one embodiment, the nucleotide sequence of the invention comprises the approximately 9.7 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-21835.

In another embodiment, the nucleotide sequence of the invention comprises the approximately 38 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-30077.

In still another embodiment, the nucleotide sequence of the invention comprises the approximately 22.2 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-30078.

According to one embodiment of the invention, the toxins resulting from expression of the nucleic acid molecules of the invention have activity against Lepidopteran insects. Preferably, according to this embodiment, the toxins have activity against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

According to another embodiment of the invention, the toxins resulting from expression of the nucleic acid molecule of the invention have activity against Lepidopteran and Coleopteran insects. Preferably, according to this embodiment, the toxins have insecticidal activity against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In another aspect, the present invention provides an isolated nucleic acid molecule comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11, wherein expression of the nucleic acid molecule results in at least one toxin that is active against insects.

In one embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

In another embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 15,171-18,035 of SEQ ID NO:11.

In still another embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 31,393-35,838 of SEQ ID NO:11.

In a further aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence from *Photorhabdus luminescens* selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 66-1898 of SEQ ID NO:11, nucleotides 2416-9909 of SEQ ID NO:11, the complement of nucleotides 2817-3395 of SEQ ID NO:11, nucleotides 9966-14,633 of SEQ ID NO:11, nucleotides 14,699-15,007 of SEQ ID NO:11, nucleotides 15,171-18,035 of SEQ ID NO:11, the complement of nucleotides 17,072-17,398 of SEQ ID NO:11, the complement of nucleotides 18,235-19,167 of SEQ ID NO:11, the complement of nucleotides 19,385-20,116 of SEQ ID NO:11, the complement of nucleotides 20,217-20,963 of SEQ ID NO:11, the complement of nucleotides 22,172-23,086 of SEQ ID NO:11, nucleotides 23,768-31,336 of SEQ ID NO:11, nucleotides 31,393-35,838 of SEQ ID NO:11, the complement of nucleotides 35,383-35,709 of SEQ ID NO:11, the complement of nucleotides 36,032-36,661 of SEQ ID NO:11, and the complement of nucleotides 36,654-37,781 of SEQ ID NO:11.

The present invention also provides a chimeric gene comprising a heterologous promoter sequence operatively linked to the nucleic acid molecule of the invention. Further, the present invention provides a recombinant vector comprising such a chimeric gene. Still further, the present invention provides a host cell comprising such a chimeric gene. A host cell according to this aspect of the invention may be a bacterial cell, a yeast cell, or a plant

cell, preferably a plant cell. Even further, the present invention provides a plant comprising such a plant cell. Preferably, the plant is maize.

In yet another aspect, the present invention provides toxins produced by the expression of DNA molecules of the present invention.

According to one embodiment, the toxins of the invention have activity against Lepidopteran insects, preferably against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

According to another embodiment, the toxins of the invention have activity against Lepidopteran and Coleopteran insects, preferably against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In one embodiment, the toxins are produced by the *E. coli* strain designated as NRRL accession number B-21835.

In another embodiment, the toxins are produced by *E. coli* strain designated as NRRL accession number B-30077.

In still another embodiment, the toxins are produced by *E. coli* strain designated as NRRL accession number B-30078.

In one embodiment, a toxin of the invention comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:2-6.

In another embodiment, a toxin of the invention comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:12-14.

The present invention also provides a composition comprising an insecticidally effective amount of a toxin according to the invention.

In another aspect, the present invention provides a method of producing a toxin that is active against insects, comprising: (a) obtaining a host cell comprising a chimeric gene, which itself comprises a heterologous promoter sequence operatively linked to the nucleic acid molecule of the invention; and (b) expressing the nucleic acid molecule in the cell, which results in at least one toxin that is active against insects.

In a further aspect, the present invention provides a method of producing an insect-resistant plant, comprising introducing a nucleic acid molecule of the invention into the plant, wherein the nucleic acid molecule is expressible in the plant in an effective amount to control insects. According to one embodiment, the insects are Lepidopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm). According to another embodiment, the insects are Lepidopteran and Coleopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa. decimlineata* (Colorado Potato Beetle).

In still a further aspect, the present invention provides a method of controlling insects comprising delivering to the insects an effective amount of a toxin according to the present invention. According to one embodiment, the insects are Lepidopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm). According to another embodiment, the insects are Lepidopteran and Coleopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle). Preferably, the toxin is delivered to the insects orally.

Yet another aspect of the present invention is the provision of a method for mutagenizing a nucleic acid molecule according to the present invention, wherein the nucleic acid molecule has been cleaved into population of double-stranded random fragments of a desired size, comprising: (a) adding to the population of double-stranded random fragments one or more single- or double-stranded oligonucleotides, wherein the oligonucleotides each comprise an area of identity and an area of heterology to a double-stranded template polynucleotide; (b) denaturing the resultant mixture of double-stranded

random fragments and oligonucleotides into single-stranded fragments; (c) incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of the single-stranded fragments at the areas of identity to form pairs of annealed fragments, the areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and (d) repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and wherein the further cycle forms a further mutagenized double-stranded polynucleotide.

Other aspects and advantages of the present invention will become apparent to those skilled in the art from a study of the following description of the invention and non-limiting examples.

DEFINITIONS

"Activity" of the toxins of the invention is meant that the toxins function as orally active insect control agents, have a toxic effect, or are able to disrupt or deter insect feeding, which may or may not cause death of the insect. When a toxin of the invention is delivered to the insect, the result is typically death of the insect, or the insect does not feed upon the source that makes the toxin available to the insect.

"Associated with / operatively linked" refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

A "chimeric gene" is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulator nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulator nucleic acid sequence of the chimeric gene is not normally operatively linked to the associated nucleic acid sequence as found in nature.

A "coding sequence" is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

To "control" insects means to inhibit, through a toxic effect, the ability of insect pests to survive, grow, feed, and/or reproduce, or to limit insect-related damage or loss in crop plants. To "control" insects may or may not mean killing the insects, although it preferably means killing the insects.

To "deliver" a toxin means that the toxin comes in contact with an insect, resulting in toxic effect and control of the insect. The toxin can be delivered in many recognized ways, e.g., orally by ingestion by the insect or by contact with the insect via transgenic plant expression, formulated protein composition(s), sprayable protein composition(s), a bait matrix, or any other art-recognized toxin delivery system.

"Expression cassette" as used herein means a nucleic acid sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular nucleic acid sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue, or organ, or stage of development.

A "gene" is a defined region that is located within a genome and that, besides the aforementioned coding nucleic acid sequence, comprises other, primarily regulatory, nucleic acid sequences responsible for the control of the expression, that is to say the transcription and translation, of the coding portion. A gene may also comprise other 5' and 3'

untranslated sequences and termination sequences. Further elements that may be present are, for example, introns.

"Gene of interest" refers to any gene which, when transferred to a plant, confers upon the plant a desired characteristic such as antibiotic resistance, virus resistance, insect resistance, disease resistance, or resistance to other pests, herbicide tolerance, improved nutritional value, improved performance in an industrial process or altered reproductive capability. The "gene of interest" may also be one that is transferred to plants for the production of commercially valuable enzymes or metabolites in the plant.

A "heterologous" nucleic acid sequence is a nucleic acid sequence not naturally associated with a host cell into which it is introduced, including non-naturally occurring multiple copies of a naturally occurring nucleic acid sequence.

A "homologous" nucleic acid sequence is a nucleic acid sequence naturally associated with a host cell into which it is introduced.

"Homologous recombination" is the reciprocal exchange of nucleic acid fragments between homologous nucleic acid molecules.

"Insecticidal" is defined as a toxic biological activity capable of controlling insects, preferably by killing them.

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

An "isolated" nucleic acid molecule or an isolated enzyme is a nucleic acid molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated nucleic acid molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, a recombinant host cell.

A "nucleic acid molecule" or "nucleic acid sequence" is a linear segment of single- or double-stranded DNA or RNA that can be isolated from any source. In the context of the present invention, the nucleic acid molecule is preferably a segment of DNA.

"ORF" means open reading frame.

A "plant" is any plant at any stage of development, particularly a seed plant.

A "plant cell" is a structural and physiological unit of a plant, comprising a protoplast and a cell wall. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, plant tissue, a plant organ, or a whole plant.

"Plant cell culture" means cultures of plant units such as, for example, protoplasts, cell culture cells, cells in plant tissues, pollen, pollen tubes, ovules, embryo sacs, zygotes and embryos at various stages of development.

"Plant material" refers to leaves, stems, roots, flowers or flower parts, fruits, pollen, egg cells, zygotes, seeds, cuttings, cell or tissue cultures, or any other part or product of a plant.

A "plant organ" is a distinct and visibly structured and differentiated part of a plant such as a root, stem, leaf, flower bud, or embryo.

"Plant tissue" as used herein means a group of plant cells organized into a structural and functional unit. Any tissue of a plant *in planta* or in culture is included. This term includes, but is not limited to, whole plants, plant organs, plant seeds, tissue culture and any groups of plant cells organized into structural and/or functional units. The use of this term in conjunction with, or in the absence of, any specific type of plant tissue as listed above or otherwise embraced by this definition is not intended to be exclusive of any other type of plant tissue.

A "promoter" is an untranslated DNA sequence upstream of the coding region that contains the binding site for RNA polymerase II and initiates transcription of the DNA. The promoter region may also include other elements that act as regulators of gene expression.

A "protoplast" is an isolated plant cell without a cell wall or with only parts of the cell wall.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operably linked to the nucleotide sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence corresponding to a reference nucleotide sequence, wherein the corresponding sequence encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by the reference nucleotide sequence, e.g. where only changes in amino acids not affecting the polypeptide function occur. Desirably the substantially similar nucleotide sequence encodes the polypeptide encoded by the reference nucleotide sequence. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence desirably is at least 80%, more desirably at least 85%, preferably at least 90%, more preferably at least 95%, still more preferably at least 99%. A nucleotide sequence

"substantially similar" to reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

"Synthetic" refers to a nucleotide sequence comprising structural characters that are not present in the natural sequence. For example, an artificial sequence that resembles more closely the G+C content and the normal codon distribution of dicot and/or monocot genes is said to be synthetic.

"Transformation" is a process for introducing heterologous nucleic acid into a host cell or organism. In particular, "transformation" means the stable integration of a DNA molecule into the genome of an organism of interest.

"Transformed / transgenic / recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed", "non-transgenic", or "non-recombinant" host refers to a wild-type organism, e.g., a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

Nucleotides are indicated by their bases by the following standard abbreviations: adenine (A), cytosine (C), thymine (T), and guanine (G). Amino acids are likewise indicated by the following standard abbreviations: alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C), glutamine (Gln; Q), glutamic acid (Glu; E), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V). Furthermore, (Xaa; X) represents any amino acid.

BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

SEQ ID NO:1 is the sequence of the approximately 9.7 kb DNA fragment comprised in pCIB9359-7 which comprises the following ORFs at the specified nucleotide positions:

Name	Start	End
orf1	412	1665
orf2	1686	2447
orf3	2758	3318
orf4	3342	4118
orf5	4515	9269

SEQ ID NO:2 is the sequence of the ~46.4 kDa protein encoded by orf1 of SEQ ID NO:1.
SEQ ID NO:3 is the sequence of the ~28.1 kDa protein encoded by orf2 of SEQ ID NO:1.
SEQ ID NO:4 is the sequence of the ~20.7 kDa protein encoded by orf3 of SEQ ID NO:1.
SEQ ID NO:5 is the sequence of the ~28.7 kDa protein encoded by orf4 of SEQ ID NO:1.
SEQ ID NO:6 is the sequence of the ~176 kDa protein encoded by orf5 of SEQ ID NO:1.
SEQ ID NOs:7-10 are oligonucleotides.
SEQ ID NO:11 is the sequence of the approximately 38 kb DNA fragment comprised in pNOV2400, which comprises the following ORFs at the specified nucleotide positions (descending numbers and "C" indicates that the ORF is on the complementary strand):

Name	Start	End	
orf7	66	1898	(partial sequence)
hph3	2416	9909	
orf18	3395	2817	C
orf4	9966	14,633	
orf19	14,699	15,007	
orf5	15,171	18,035	
orf22	17,398	17,072	C
orf10	19,167	18,235	C
orf14	20,116	19,385	C
orf13	20,963	20,217	C
orf11	23,086	22,172	C
hph2	23,768	31,336	
orf2	31,393	35,838	

orf21	35,709	35,383	C
orf16	36,661	36,032	C
orf8	37,781	36,654	C

SEQ ID NO:11 also includes the following restriction sites, some of which are used in the subcloning steps set forth in Example 17:

Restriction Site	Nucleotide Position(s)
*Acc*III	2835
*Bam*HI	18,915
*Bsm*BI	11,350
*Bst*1107I	29,684
*Eag*I	13,590; 31,481
*Eco*721	34,474
*Mlu*I	2444; 5116; 9327; 26,204
*Not*I	13,589
*Pac*I	9915; 23,353; 37,888
*Pvu*I	8816
*Sap*I	35,248
*Sex*AI	28,946
*Sgf*I	8815
*Spe*I	2157; 3769; 7831; 11,168
*Sph*I	755
*Stu*I	35,690
*Tth*111I	21,443

SEQ ID NO:12 is the sequence of the protein encoded by orf5 of SEQ ID NO:11.
SEQ ID NO:13 is the sequence of the protein encoded by hph2 of SEQ ID NO:11.
SEQ ID NO:14 is the sequence of the protein encoded by orf2 of SEQ ID NO:11.
SEQ ID NOs:15-22 are oligonucleotides.

DEPOSITS

The following material has been deposited with the Agricultural Research Service, Patent Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604, under the terms of the Budapest Treaty on the International Recognition of the Deposit of

Microorganisms for the Purposes of Patent Procedure. All restrictions on the availability of the deposited material will be irrevocably removed upon the granting of a patent.

Clone	Accession Number	Date of Deposit
pCIB9359-7	NRRL B-21835	September 17, 1997
pNOV2400	NRRL B-30077	December 3, 1998
pNOV1001	NRRL B-30078	December 3, 1998

Novel Nucleic Acid Sequences whose Expression Results in Insecticidal Toxins

This invention relates to nucleic acid sequences whose expression results in novel toxins, and to the making and using of the toxins to control insect pests. The nucleic acid sequences are derived from *Photorhabdus luminescens*, a member of the *Enterobacteriaceae* family. *P. luminescens* is a symbiotic bacterium of nematodes of the genus *Heterorhabditis*. The nematodes colonize insect larva, kill them, and their offspring feed on the dead larvae. The insecticidal activity is actually produced by the symbiotic *P. luminescens* bacteria. The inventors are the first to isolate the nucleic acid sequences of the present invention from *P. luminescens* (ATCC strain number 29999). The expression of the nucleic acid sequences of the present invention results in toxins that can be used to control Lepidopteran insects such as *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Manduca sexta* (Tobacco Hornworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), as well as Coleopteran insects such as *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), *Diabrotica longicornis barberi* (Northern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In one preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the approximately 9.7 kb nucleic acid sequence set forth in SEQ ID NO:1, whose expression results in insect control activity (further illustrated in Examples 1-11). Five open reading frames (ORFs) are present in the nucleic acid sequence set forth in SEQ ID NO:1, coding for proteins of predicted sizes 45 kDa, 28 kDa, 21 kDA, 29 kDa, and 176 kDa. The five ORFs are arranged in an operon-like structure. When expressed in a heterologous host, the ~ 9.7 kb DNA fragment from *P.*

luminescens results in insect control activity against Lepidopterans such as *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), showing that expression of the ~ 9.7 kb nucleotide sequence set forth in SEQ ID NO:1 is necessary and sufficient for such insect control activity. In a preferred embodiment, the invention encompasses a DNA molecule, whose expression results in an insecticidal toxin, which is deposited in the *E. coli* strain pCIB9359-7 (NRRL accession number B-21835).

In another preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the approximately 38 kb nucleic acid fragment set forth in SEQ ID NO:11 and deposited in the *E. coli* strain pNOV2400 (NRRL accession number B-30077), whose expression results in insect control activity (see Examples 12-18). In a more preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the ~ 22 kb DNA fragment deposited in the *E. coli* strain pNOV1001 (NRRL accession number B-30078), whose expression results in insect control activity. In a most preferred embodiment, the invention encompasses isolated nucleic acid molecules comprising nucleotide sequences substantially similar to the three ORFs corresponding to nucleotides 23,768-31,336 (hph2), 31,393-35,838 (orf2), and 15,171-18,035 (orf5) of the DNA fragment set forth in SEQ ID NO:11, as well as the proteins encoded thereby. When co-expressed in a heterologous host, these three ORFs result in insect control activity against Lepidopterans such as *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), as well as against Coleopterans such as *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle), showing that co-expression of these three ORFs (hph2, orf2, and orf5) is necessary and sufficient for such insect control activity.

The present invention also encompasses recombinant vectors comprising the nucleic acid sequences of this invention. In such vectors, the nucleic acid sequences are preferably comprised in expression cassettes comprising regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise promoter and termination signals and preferably also

comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, preferably as extrachromosomal molecules, and are therefore used to amplify the nucleic acid sequences of this invention in the host cells. In one embodiment, host cells for such vectors are microorganisms, such as bacteria, in particular *E.coli*. In another embodiment, host cells for such recombinant vectors are endophytes or epiphytes. A preferred host cell for such vectors is a eukaryotic cell, such as a yeast, a plant cell, or an insect cell. Plant cells such as maize cells are most preferred host cells. In another preferred embodiment, such vectors are viral vectors and are used for replication of the nucleotide sequences in particular host cells, e.g. insect cells or plant cells. Recombinant vectors are also used for transformation of the nucleotide sequences of this invention into host cells, whereby the nucleotide sequences are stably integrated into the DNA of such host cells. In one, such host cells are prokaryotic cells. In a preferred embodiment, such host cells are eukaryotic cells, such as yeast cells, insect cells, or plant cells. In a most preferred embodiment, the host cells are plant cells, such as maize cells.

In preferred embodiments, the insecticidal toxins of the invention each comprise at least one polypeptide encoded by a nucleotide sequence of the invention. In another preferred embodiment, the insecticidal toxins are produced from a purified strain of *P. luminescens*, such the strain with ATTC accession number 29999. The toxins of the present invention have insect control activity when tested against insect pests in bioassays; and these properties of the insecticidal toxins are further illustrated in Examples 1-18. The insecticidal toxins desribed in the present invention are further characterized in that their molecular weights are larger than 6,000, as found by size fractionation experiments. The insecticidal toxins retain full insectidical activity after being stored at 4°C for 2 weeks. One is also shown to retain its full insecticidal activity after being freeze-dried and stored at 22°C for 2 weeks. However, the insecticidal toxins of the invention lose their insecticidal activity after incubation for 5 minutes at 100°C.

In further embodiments, the nucleotide sequences of the invention can be modified by incorporation of random mutations in a technique known as *in-vitro* recombination or DNA shuffling. This technique is described in Stemmer et al., Nature 370: 389-391 (1994) and US Patent 5,605,793, which are incorporated herein by reference. Millions of mutant copies of a nucleotide sequence are produced based on an original nucleotide sequence of

this invention and variants with improved properties, such as increased insecticidal activity, enhanced stability, or different specificity or range of target insect pests are recovered. The method encompasses forming a mutagenized double-stranded polynucleotide from a template double-stranded polynucleotide comprising a nucleotide sequence of this invention, wherein the template double-stranded polynucleotide has been cleaved into double-stranded-random fragments of a desired size, and comprises the steps of adding to the resultant population of double-stranded random fragments one or more single or double-stranded oligonucleotides, wherein said oligonucleotides comprise an area of identity and an area of heterology to the double-stranded template polynucleotide; denaturing the resultant mixture of double-stranded random fragments and oligonucleotides into single-stranded fragments; incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of said single-stranded fragments at said areas of identity to form pairs of annealed fragments, said areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and the further cycle forms a further mutagenized double-stranded polynucleotide. In a preferred embodiment, the concentration of a single species of double-stranded random fragment in the population of double-stranded random fragments is less than 1% by weight of the total DNA. In a further preferred embodiment, the template double-stranded polynucleotide comprises at least about 100 species of polynucleotides. In another preferred embodiment, the size of the double-stranded random fragments is from about 5 bp to 5 kb. In a further preferred embodiment, the fourth step of the method comprises repeating the second and the third steps for at least 10 cycles.

Expression of the Nucleotide Sequences in Heterologous Microbial Hosts

As biological insect control agents, the insecticidal toxins are produced by expression of the nucleotide sequences in heterologous host cells capable of expressing the nucleotide sequences. In a first embodiment, *P. luminescens* cells comprising modifications of at least one nucleotide sequence of this invention at its chromosomal location are described. Such modifications encompass mutations or deletions of existing regulatory elements, thus leading to altered expression of the nucleotide sequence, or the incorporation of new regulatory elements controlling the expression of the nucleotide sequence. In another

embodiment, additional copies of one or more of the nucleotide sequences are added to *P. luminescens* cells either by insertion into the chromosome or by introduction of extrachromosomally replicating molecules containing the nucleotide sequences.

In another embodiment, at least one of the nucleotide sequences of the invention is inserted into an appropriate expression cassette, comprising a promoter and termination signals. Expression of the nucleotide sequence is constitutive, or an inducible promoter responding to various types of stimuli to initiate transcription is used. In a preferred embodiment, the cell in which the toxin is expressed is a microorganism, such as a virus, a bacteria, or a fungus. In a preferred embodiment, a virus, such as a baculovirus, contains a nucleotide sequence of the invention in its genome and expresses large amounts of the corresponding insecticidal toxin after infection of appropriate eukaryotic cells that are suitable for virus replication and expression of the nucleotide sequence. The insecticidal toxin thus produced is used as an insecticidal agent. Alternatively, baculoviruses engineered to include the nucleotide sequence are used to infect insects *in-vivo* and kill them either by expression of the insecticidal toxin or by a combination of viral infection and expression of the insecticidal toxin.

Bacterial cells are also hosts for the expression of the nucleotide sequences of the invention. In a preferred embodiment, non-pathogenic symbiotic bacteria, which are able to live and replicate within plant tissues, so-called endophytes, or non-pathogenic symbiotic bacteria, which are capable of colonizing the phyllosphere or the rhizosphere, so-called epiphytes, are used. Such bacteria include bacteria of the genera *Agrobacterium, Alcaligenes, Azospirillum, Azotobacter, Bacillus, Clavibacter, Enterobacter, Erwinia, Flavobacter, Klebsiella, Pseudomonas, Rhizobium, Serratia, Streptomyces and Xanthomonas*. Symbiotic fungi, such as *Trichoderma* and *Gliocladium* are also possible hosts for expression of the inventive nucleotide sequences for the same purpose.

Techniques for these genetic manipulations are specific for the different available hosts and are known in the art. For example, the expression vectors pKK223-3 and pKK223-2 can be used to express heterologous genes in *E. coli*, either in transcriptional or translational fusion, behind the *tac or trc* promoter. For the expression of operons encoding multiple ORFs, the simplest procedure is to insert the operon into a vector such as pKK223-3 in transcriptional fusion, allowing the cognate ribosome binding site of the heterologous genes to be used. Techniques for overexpression in gram-positive species such as *Bacillus* are also known in the art and can be used in the context of this invention (Quax *et al. In.:*

Industrial Microorganisms: Basic and Applied Molecular Genetics, *Eds.* Baltz *et al.*, American Society for Microbiology, Washington (1993)). Alternate systems for overexpression rely for example, on yeast vectors and include the use of *Pichia*, *Saccharomyces* and *Kluyveromyces* (Sreekrishna, *In*: Industrial microorganisms: basic and applied molecular genetics, Baltz, Hegeman, and Skatrud *eds.*, American Society for Microbiology, Washington (1993); Dequin & Barre, Biotechnology 12:173-177 (1994); van den Berg *et al.*, Biotechnology 8:135-139 (1990)).

In another preferred embodiment, at least one of the described nucleotide sequences is transferred to and expressed in *Pseudomonas fluorescens* strain CGA267356 (described in the published application EU 0 472 494 and in WO 94/01561) which has biocontrol characteristics. In another preferred embodiment, a nucleotide sequence of the invention is transferred to *Pseudomonas aureofaciens* strain 30-84 which also has biocontrol characteristics. Expression in heterologous biocontrol strains requires the selection of vectors appropriate for replication in the chosen host and a suitable choice of promoter. Techniques are well known in the art for expression in gram-negative and gram-positive bacteria and fungi.

Expression of the Nucleotide Sequences in Plant Tissue

In a particularly preferred embodiment, at least one of the insecticidal toxins of the invention is expressed in a higher organism, e.g., a plant. In this case, transgenic plants expressing effective amounts of the toxins protect themselves from insect pests. When the insect starts feeding on such a transgenic plant, it also ingests the expressed toxins. This will deter the insect from further biting into the plant tissue or may even harm or kill the insect. A nucleotide sequence of the present invention is inserted into an expression cassette, which is then preferably stably integrated in the genome of said plant. In another preferred embodiment, the nucleotide sequence is included in a non-pathogenic self-replicating virus. Plants transformed in accordance with the present invention may be monocots or dicots and include, but are not limited to, maize, wheat, barley, rye, sweet potato, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, pepper, celery, squash, pumpkin, hemp, zucchini, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tomato, sorghum, sugarcane, sugarbeet, sunflower, rapeseed, clover, tobacco, carrot, cotton, alfalfa, rice,

potato, eggplant, cucumber, *Arabidopsis*, and woody plants such as coniferous and deciduous trees.

Once a desired nucleotide sequence has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques.

A nucleotide sequence of this invention is preferably expressed in transgenic plants, thus causing the biosynthesis of the corresponding toxin in the transgenic plants. In this way, transgenic plants with enhanced resistance to insects are generated. For their expression in transgenic plants, the nucleotide sequences of the invention may require modification and optimization. Although in many cases genes from microbial organisms can be expressed in plants at high levels without modification, low expression in transgenic plants may result from microbial nucleotide sequences having codons that are not preferred in plants. It is known in the art that all organisms have specific preferences for codon usage, and the codons of the nucleotide sequences described in this invention can be changed to conform with plant preferences, while maintaining the amino acids encoded thereby. Furthermore, high expression in plants is best achieved from coding sequences that have at least 35% about GC content, preferably more than about 45%, more preferably more than about 50%, and most preferably more than about 60%. Microbial nucleotide sequences which have low GC contents may express poorly in plants due to the existence of ATTTA motifs which may destabilize messages, and AATAAA motifs which may cause inappropriate polyadenylation. Although preferred gene sequences may be adequately expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.* Nucl. Acids Res. 17: 477-498 (1989)). In addition, the nucleotide sequences are screened for the existence of illegitimate splice sites that may cause message truncation. All changes required to be made within the nucleotide sequences such as those described above are made using well known techniques of site directed mutagenesis, PCR, and synthetic gene construction using the methods described in the published patent applications EP 0 385 962 (to Monsanto), EP 0 359 472 (to Lubrizol, and WO 93/07278 (to Ciba-Geigy).

For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be effective in plants. Joshi has suggested an appropriate consensus for plants

(NAR 15: 6643-6653 (1987)) and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensuses are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. Thus, expression of the nucleotide sequences of this invention in leaves, in ears, in inflorescences (*e.g.* spikes, panicles, cobs, *etc.*), in roots, and/or seedlings is preferred. In many cases, however, protection against more than one type of insect pest is sought, and thus expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the insecticidal toxins to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP 0 332 104 (to Ciba-Geigy) and US patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

A preferred category of promoters is that which is wound inducible. Numerous promoters have been described which are expressed at wound sites and also at the sites of phytopathogen infection. Ideally, such a promoter should only be active locally at the sites of infection, and in this way the insecticidal toxins only accumulate in cells which need to synthesize the insecticidal toxins to kill the invading insect pest. Preferred promoters of this kind include those described by Stanford *et al.* Mol. Gen. Genet. 215: 200-208 (1989), Xu *et al.* Plant Molec. Biol. 22: 573-588 (1993), Logemann *et al.* Plant Cell 1: 151-158 (1989),

Rohrmeier & Lehle, Plant Molec. Biol. 22: 783-792 (1993), Firek *et al.* Plant Molec. Biol. 22: 129-142 (1993), and Warner *et al.* Plant J. 3: 191-201 (1993).

Preferred tissue specific expression patterns include green tissue specific, root specific, stem specific, and flower specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, Plant Molec. Biol. 12: 579-589 (1989)). A preferred promoter for root specific expression is that described by de Framond (FEBS 290: 103-106 (1991); EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in US patent 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Especially preferred embodiments of the invention are transgenic plants expressing at least one of the nucleotide sequences of the invention in a root-preferred or root-specific fashion. Further preferred embodiments are transgenic plants expressing the nucleotide sequences in a wound-inducible or pathogen infection-inducible manner.

In addition to the selection of a suitable promoter, constructions for expression of an insecticidal toxin in plants require an appropriate transcription terminator to be attached downstream of the heterologous nucleotide sequence. Several such terminators are available and known in the art (*e.g. tm1* from CaMV, E9 from *rbcS*). Any available terminator known to function in plants can be used in the context of this invention.

Numerous other sequences can be incorporated into expression cassettes described in this invention. These include sequences which have been shown to enhance expression such as intron sequences (*e.g.* from *Adh1* and *bronze1*) and viral leader sequences (*e.g.* from TMV, MCMV and AMV).

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle may be preferred. Subcellular localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the

nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

Vectors suitable for plant transformation are described elsewhere in this specification. For *Agrobacterium*-mediated transformation, binary vectors or vectors carrying at least one T-DNA border sequence are suitable, whereas for direct gene transfer any vector is suitable and linear DNA containing only the construction of interest may be preferred. In the case of direct gene transfer, transformation with a single DNA species or co-transformation can be used (Schocher *et al.* Biotechnology 4: 1093-1096 (1986)). For both direct gene transfer and *Agrobacterium*-mediated transfer, transformation is usually (but not necessarily) undertaken with a selectable marker which may provide resistance to an antibiotic (kanamycin, hygromycin or methotrexate) or a herbicide (basta). The choice of selectable marker is not, however, critical to the invention.

In another preferred embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. A major advantage of plastid transformation is that plastids are generally capable of expressing bacterial genes without substantial modification, and plastids are capable of expressing multiple open reading frames under control of a single promoter. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride *et al.* (1994) Proc. Natl. Acad. Sci. USA 91, 7301-7305. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate homologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab, Z., Hajdukiewicz, P., and Maliga, P. (1990) Proc. Natl. Acad. Sci. USA 87, 8526-8530; Staub, J. M., and Maliga, P. (1992) Plant Cell 4, 39-45). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub, J.M., and Maliga, P. (1993) *EMBO J.* 12, 601-606). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial

aadA gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab, Z., and Maliga, P. (1993) *Proc. Natl. Acad. Sci. USA* 90, 913-917). Previously, this marker had been used successfully for high-frequency transformation of the plastid genome of the green alga *Chlamydomonas reinhardtii* (Goldschmidt-Clermont, M. (1991) *Nucl. Acids Res.* 19: 4083-4089). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid expression, in which genes are inserted by homologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Formulation of Insecticidal Compositions

The invention also includes compositions comprising at least one of the insecticidal toxins of the present invention. In order to effectively control insect pests such compositions preferably contain sufficient amounts of toxin. Such amounts vary depending on the crop to be protected, on the particular pest to be targeted, and on the environmental conditions, such as humidity, temperature or type of soil. In a preferred embodiment, compositions comprising the insecticidal toxins comprise host cells expressing the toxins without additional purification. In another preferred embodiment, the cells expressing the insecticidal toxins are lyophilized prior to their use as an insecticidal agent. In another embodiment, the insecticidal toxins are engineered to be secreted from the host cells. In cases where purification of the toxins from the host cells in which they are expressed is desired, various degrees of purification of the insecticidal toxins are reached.

The present invention further embraces the preparation of compositions comprising at least one insecticidal toxin of the present invention, which is homogeneously mixed with one or more compounds or groups of compounds described herein. The present invention also relates to methods of treating plants, which comprise application of the insecticidal toxins or compositions containing the insecticidal toxins, to plants. The insecticidal toxins

can be applied to the crop area in the form of compositions or plant to be treated, simultaneously or in succession, with further compounds. These compounds can be both fertilizers or micronutrient donors or other preparations that influence plant growth. They can also be selective herbicides, insecticides, fungicides, bactericides, nematicides, molluscicides or mixtures of several of these preparations, if desired together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers.

A preferred method of applying insecticidal toxins of the present invention is by spraying to the environment hosting the insect pest like the soil, water, or foliage of plants. The number of applications and the rate of application depend on the type and intensity of infestation by the insect pest. The insecticidal toxins can also penetrate the plant through the roots via the soil (systemic action) by impregnating the locus of the plant with a liquid composition, or by applying the compounds in solid form to the soil, e.g. in granular form (soil application). The insecticidal toxins may also be applied to seeds (coating) by impregnating the seeds either with a liquid formulation containing insecticidal toxins, or coating them with a solid formulation. In special cases, further types of application are also possible, for example, selective treatment of the plant stems or buds. The insecticidal toxins can also be provided as bait located above or below the ground.

The insecticidal toxins are used in unmodified form or, preferably, together with the adjuvants conventionally employed in the art of formulation, and are therefore formulated in known manner to emulsifiable concentrates, coatable pastes, directly sprayable or dilutable solutions, dilute emulsions, wettable powders, soluble powders, dusts, granulates, and also encapsulations, for example, in polymer substances. Like the nature of the compositions, the methods of application, such as spraying, atomizing, dusting, scattering or pouring, are chosen in accordance with the intended objectives and the prevailing circumstances.

The formulations, compositions or preparations containing the insecticidal toxins and, where appropriate, a solid or liquid adjuvant, are prepared in known manner, for example by homogeneously mixing and/or grinding the insecticidal toxins with extenders, for example solvents, solid carriers and, where appropriate, surface-active compounds (surfactants).

Suitable solvents include aromatic hydrocarbons, preferably the fractions having 8 to 12 carbon atoms, for example, xylene mixtures or substituted naphthalenes, phthalates

such as dibutyl phthalate or dioctyl phthalate, aliphatic hydrocarbons such as cyclohexane or paraffins, alcohols and glycols and their ethers and esters, such as ethanol, ethylene glycol monomethyl or monoethyl ether, ketones such as cyclohexanone, strongly polar solvents such as N-methyl-2-pyrrolidone, dimethyl sulfoxide or dimethyl formamide, as well as epoxidized vegetable oils such as epoxidized coconut oil or soybean oil or water.

The solid carriers used e.g. for dusts and dispersible powders, are normally natural mineral fillers such as calcite, talcum, kaolin, montmorillonite or attapulgite. In order to improve the physical properties it is also possible to add highly dispersed silicic acid or highly dispersed absorbent polymers. Suitable granulated adsorptive carriers are porous types, for example pumice, broken brick, sepiolite or bentonite; and suitable nonsorbent carriers are materials such as calcite or sand. In addition, a great number of pregranulated materials of inorganic or organic nature can be used, e.g. especially dolomite or pulverized plant residues.

Suitable surface-active compounds are nonionic, cationic and/or anionic surfactants having good emulsifying, dispersing and wetting properties. The term "surfactants" will also be understood as comprising mixtures of surfactants. Suitable anionic surfactants can be both water-soluble soaps and water-soluble synthetic surface-active compounds.

Suitable soaps are the alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts of higher fatty acids (chains of 10 to 22 carbon atoms), for example the sodium or potassium salts of oleic or stearic acid, or of natural fatty acid mixtures which can be obtained for example from coconut oil or tallow oil. The fatty acid methyltaurin salts may also be used.

More frequently, however, so-called synthetic surfactants are used, especially fatty sulfonates, fatty sulfates, sulfonated benzimidazole derivatives or alkylarylsulfonates.

The fatty sulfonates or sulfates are usually in the form of alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts and have a 8 to 22 carbon alkyl radical which also includes the alkyl moiety of alkyl radicals, for example, the sodium or calcium salt of lignonsulfonic acid, of dodecylsulfate or of a mixture of fatty alcohol sulfates obtained from natural fatty acids. These compounds also comprise the salts of sulfuric acid esters and sulfonic acids of fatty alcohol/ethylene oxide adducts. The sulfonated benzimidazole derivatives preferably contain 2 sulfonic acid groups and one fatty acid radical containing 8 to 22 carbon atoms. Examples of alkylarylsulfonates are the sodium, calcium or triethanolamine salts of dodecylbenzenesulfonic acid, dibutylnapthalenesulfonic acid, or of a naphthalenesulfonic acid/formaldehyde

condensation product. Also suitable are corresponding phosphates, e.g. salts of the phosphoric acid ester of an adduct of p-nonylphenol with 4 to 14 moles of ethylene oxide.

Non-ionic surfactants are preferably polyglycol ether derivatives of aliphatic or cycloaliphatic alcohols, or saturated or unsaturated fatty acids and alkylphenols, said derivatives containing 3 to 30 glycol ether groups and 8 to 20 carbon atoms in the (aliphatic) hydrocarbon moiety and 6 to 18 carbon atoms in the alkyl moiety of the alkylphenols.

Further suitable non-ionic surfactants are the water-soluble adducts of polyethylene oxide with polypropylene glycol, ethylenediamine propylene glycol and alkylpolypropylene glycol containing 1 to 10 carbon atoms in the alkyl chain, which adducts contain 20 to 250 ethylene glycol ether groups and 10 to 100 propylene glycol ether groups. These compounds usually contain 1 to 5 ethylene glycol units per propylene glycol unit.

Representative examples of non-ionic surfactants are nonylphenolpolyethoxyethanols, castor oil polyglycol ethers, polypropylene/polyethylene oxide adducts, tributylphenoxypolyethoxyethanol, polyethylene glycol and octylphenoxyethoxyethanol. Fatty acid esters of polyoxyethylene sorbitan and polyoxyethylene sorbitan trioleate are also suitable non-ionic surfactants.

Cationic surfactants are preferably quaternary ammonium salts which have, as N-substituent, at least one C8-C22 alkyl radical and, as further substituents, lower unsubstituted or halogenated alkyl, benzyl or lower hydroxyalkyl radicals. The salts are preferably in the form of halides, methylsulfates or ethylsulfates, e.g. stearyltrimethylammonium chloride or benzyldi(2-chloroethyl)ethylammonium bromide.

The surfactants customarily employed in the art of formulation are described, for example, in "McCutcheon's Detergents and Emulsifiers Annual," MC Publishing Corp. Ringwood, New Jersey, 1979, and Sisely and Wood, "Encyclopedia of Surface Active Agents," Chemical Publishing Co., Inc. New York, 1980.

EXAMPLES

The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified. Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Ausubel (ed.), Current Protocols in Molecular Biology, John Wiley and Sons, Inc. (1994); T. Maniatis, E. F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor laboratory, Cold Spring Harbor, NY (1989); and by T.J. Silhavy, M.L. Berman, and L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984).

A. Isolation Of Nucleotide Sequences Whose Expression Results In Toxins Active Against Lepidopteran Insects

Example 1: Construction of Cosmid Library from *Photorhabdus luminescens*

Photorhabdus luminescens strain ATCC 29999 is grown in nutrient broth at 25°C for three days as described in the ATCC protocol for bioassay. The culture is grown for 24 hours for DNA isolation. Total DNA is isolated by treating freshly grown cells resuspended in 100 mM Tris pH 8, 10 mM EDTA with 2 mg/ml lysozyme for 30 minutes at 37°C. Proteinase K is added to a final concentration of 100 mg/ml, SDS is added to a final concentration of 0.5% SDS and the sample is incubated at 45°C. After the solution becomes clear and viscous, the SDS concentration is raised to 1%, and 300 mM NaCl and an equal volume of phenol-chloroform-isoamyl alcohol are added, mixed gently for 5 minutes and centrifuged at 3K. The phenol-chloroform-isoamyl alcohol extraction is repeated twice. The aqueous phase is mixed with 0.7 volumes isopropanol, and the sample is centrifuged. The pellet is washed 3 times with 70% ethanol and the nucleic acids are gently resuspended in 0.5X TE.

The DNA is treated with 0.3 units of *Sau3A* per mg DNA at 37°C for 3.5 minutes in 100 ml volume containing a total of 6 mg DNA. The reaction is then heated for 30 minutes at 65°C to inactivate the enzyme. Then 2 units of Calf Intestinal Alkaline Phosphatase are added and incubated for 30 minutes at 37°C. The sample is mixed with an equal volume of

phenol-chloroform-isoamyl alcohol and centrifuged. The aqueous phase is removed, precipitated with 0.7 volume isopropanol and centrifuged. The supernatant is transferred to a fresh tube, precipitated with ethanol, and the nucleic acids are resuspended in 0.5X TE at a concentration of 100 hg/ml.

SuperCos cosmid vector (Stratagene, La Jolla, CA) is prepared as described by the supplier utilizing the *BamHI* cloning site. Prepared SuperCos at 100 hg/ml is ligated with the *Sau3A* digested *P.luminescens* DNA at a molar ratio of 2:1 in a 5 ml volume overnight at 6°C. The ligation mixture is packaged using Gigapack XL III (Stratagene), as described by the supplier. Packaged phages are used to infect XL-1MR (Stratagene) cells as described by the supplier. The cosmid library is plated on L-agar with 50 mg/ml kanamycin and incubated 16 hours at 37°C. 500 colonies are patched onto fresh L-kan plates at 50 colonies per plate. From the other plates the cells are washed off with L broth and mixed with 20% glycerol and frozen at -80°C.

Example 2: Insect Bioassays

Plutella xylostella bioassays are performed by aliquoting of 50 µl of the *E. coli* culture on the solid artificial *Plutella xylostella* diet (Biever and Boldt, *Annals of Entomological Society of America*, 1971; Shelton et al., *J. Ent. Sci.* 26:17). 4 ml of the diet is poured into 1 oz. clear plastic cups (Bioserve product #9051). 5 neonate *P. xylostella* from a diet adapted lab colony are placed in each diet-containing cup and then covered with a white paper lid (Bioserve product #9049). 10 larvae are assayed per concentration. Trays of cups are placed in an incubator for 3 days at 72°F with a 14:10 (hours) light:dark cycle. Then, the number of live larvae in each cup is recorded. Bioassays for other insects are performed as described for *Plutella xylostella*, but using the diet required by the insect to be tested.

The broth of *P. luminescens* undiluted and diluted 1:100 gives 100% mortality against *P. xylostella*. The broth of *P. luminescens* also gives 100% mortality against *Diabrotica virgifera virgifera*. Three clones with activity against *P. xylostella* and *Heliothis virescens* are obtained after screening 500 *E. coli* clones by insect bioassay. These cosmid clones are given the numbers pCIB9349, pCIB9350, and pCIB9351.

Example 3: Isolation of the Nucl otid Sequence Responsible for Insect C ntrol Activity from Clones pCIB9349, pCIB9350, and pCIB9351

The three clones pCIB9349, pCIB9350 and pCIB9351 are found to be overlapping cosmids by restriction enzyme mapping. After digestion with *Pacl*, clones pCIB9349 and pCIB9351 give two DNA fragments each, and pCIB9350 gives three DNA fragments. Each fragment is isolated and is self-ligated. The enzyme *Pacl* does not cut the SuperCos vector; therefore, only fragments linked to it are re-isolated. The ligation mixtures are transformed into DH5α *E. coli* cells. Isolated transformed bacterial colonies are grown in L broth with 50 µg/ml kanamycin, and plasmid DNA is isolated by using the alkaline miniprep protocol as described in Sambrook, et al. DNA is digested with *NotI/PacI* and two clones, pCIB9355 and pCIB9356, are found by bioassay to still contain the insecticidal activity. Clone pCIB9355 is digested with *Not*I and a 17 kb and a 4 kb DNA fragment are generated. The 17 kb fragment is isolated and ligated into Bluescript vector previously cut with *Not*I and transformed into DH5α *E. coli* cells. The isolated transformed bacterial colonies are grown as described and plasmid DNA is isolated by the alkaline miniprep protocol. A clone containing the 17 kb insert is named pCIB9359 and tested by bioassay. The results are shown in Example 5. 3 µg of the 17 kb insert is isolated and treated with 0.3 unit of *Sau3A* per µg DNA for 4, 6, and 8 minutes at 37°C, heated at 75°C for 15 minutes. The samples are pooled and ligated into pUC19 previously cut with *BamHI* and treated with calf intestinal alkaline phosphatase. The ligation is transformed into DH5α cells and plated on L agar with *Xgal/Amp* as described in Sambrook et al. and grown overnight at 37°C. White colonies are picked and grown in L broth with 100 µg/ml and plasmid DNA is isolated as previously described. DNA is digested with *EcoRI/HindIII* and novel restriction patterns are sequenced. Sequencing primers are ordered from Genosys Biotechnologies (Woodlands, TX). Sequencing is performed using the dideoxy chain-termination method. Sequencing is completed using Applied Biosystems Inc. model 377 automated DNA sequencer (Foster City, CA). Sequence is assembled using 3.0 from Gene Codes Corporation (Ann Arbor, MI).

Exampl 4: Subcloning f th 9.7 kb *EcoRI/Xbal* Fragment Fr m pCIB9359

pCIB9359 is digested with *EcoRI* and *Xbal* and the DNA is run on a 0.8% Seaplaque/TBE gel. The 9.7 kb fragment (SEQ ID NO:1) is isolated and ligated into pUC19 previously digested with *EcoRI* and *Xbal*. The ligation mixture is transformed into DH5α *E. coli* cells. Transformed bacteria are grown and plasmid DNA is isolated as previously described. The vector containing the 9.7 kb fragment in pUC19 is designated pCIB9359-7 and bioassay results are shown in Example 5.

Example 5: Bioassay Results for Cosmid Clones pCIB9359 and pCIB9359-7

Cultures of *E. coli* strains 9359 and 9359-7 containing clones pCIB9359 and pCIB9359-7, respectively, are tested for insecticidal activity against the following insects in insect bioassays:

Insects	**Clones pCIB9359 and pCIB9359-7**
Plutella xylostella (Diamondback Moth (DBM))	+++
Heliothis virescens (Tobacco Budworm (TBW))	++
Helicoverpa zea (Corn Earworm (CEW))	+++
Spodoptera exigua (Beet Armyworm (BAW))	+
Spodoptera frugiperda (Fall Armyworm (FAW))	+
Trichoplusia ni (Cabbage Looper (CL))	+++
Ostrinia nubilalis (European Corn Borer (ECB))	++
Manduca sexta (Tobacco Hornworm (THW)	na
Diabrotica virgifera (Western Corn Rootworm (WCR))	na
Agrotis ipsilon (Black Cutworm (BCW))	na

na = not active

+ = significant growth inhibition

++ = >40% mortality, but less than 100%

+++ = 100% mortality

The clones show insecticidal activity against *P. xylostella*, *H. virescens*, *H. zea*, *T. ni*, and *O. nubilalis*, and significant insect control activity against *S. exigua* and *S. frugiperda*.

Example 6: Identification of Active Region of pCIB9359-7 By Subcloning

Cultures of *E. coli* strains containing subclones of pCIB9359-7 are tested for insecticidal activity in insect bioassays against *P. xylostella*.

Restriction Fragment	**Nucleotide Position Relative to 9.7 kb *EcoRI/Xbal* fragment (SEQ ID NO:1) from pCIB9539-7 and Size in kb**		**Insecticidal Activity Against *Plutella xylostella***
EcoRI/Xbal	1 to 9712	9.7 kb	+++
EcoRV	(-912) to 2309	3.2 kb	na
HindIII	665 to 5438	4.7 kb	na
KpnI	1441 to 8137	6.9 kb	na
SacI/Xbal	2677 to 9712	7.0 kb	na

na = not active

+ = significant growth inhibition

++ = >40% mortality, but less than 100%

+++ = 100% mortality

Example 7: Characterization of pCIB9359-7 Insect Control Activity By Titration

Dilutions of a culture of *E.coli* strain 9359-7 containing pCIB9359-7 are tested for insecticidal activity in insect bioassays. Dilutions are prepared in a culture of *E.coli* XL-1 in a total volume of 100 µl and are transferred to diet cups with 5 insects per cup. The results show the percentage (%) of insect mortality.

µl 9359-7 Culture	*Px*	*Hv*	*Hz*	*Tn*
100	100	72	48	100
50	100	84	68	92
25	100	52	32	100
12.5	96	52	36	68
6.25	88	20	4	32
0	36	20	24	0

Px = P. xylostella, Hv = H. virescens, Hz = H. zea, Tn = T. ni.

Cultures of *E. coli* 9359-7 still show substantial insecticidal activity after dilution.

Example 8: Stability of pCIB9359-7 Activity

The stability of the toxins is tested after storage for 2 weeks at different temperatures and conditions. 300 ml of Luria broth containing 100 (µg/ml ampicillin is inoculated with *E. coli* strain 9359-7 and grown overnight at 37°C. Samples are placed in sterile 15 ml screw cap tubes and stored at 22°C and 4°C. Another sample is centrifuged; the supernatant is removed, freeze dried and stored at 22°C. The samples are stored under these conditions for 2 weeks and then a bioassay is conducted against *P. xylostella*. The freeze dried material is resuspended in the same volume as before. All samples are resuspended by vortexing.

Conditions	**Results**
22°C (2 weeks)	+++
4°C (2 weeks)	+++
Freeze Dried (2 weeks)	+++

na = not active; + = significant growth inhibition; ++ = >40% mortality, but less than 100%; +++ = 100% mortality

This demonstrates that the toxins retain their activity for at least two weeks at 22°C, 4°C, and freeze-dried, and are therefore very stable.

Example 9: Size Fraction of pCIB9359-7 Activity

The approximate sizes of the insecticidal toxins are determined. *P. luminescens* cosmid clones pCIB9359-7 and pUC19 in *E. coli* host DH5α are grown in media consisting of 50% Terrific broth and 50% Luria broth, supplemented with 50 µg/ml ampicillin. Cultures (three tubes of each strain) are inoculated into 3 ml of the above media in culture tubes and incubated on a roller wheel overnight at 37°C. Cultures of each strain are combined and sonicated using a Branson Model 450 Sonicator, micro tip, for approximately six 10 second cycles with cooling on ice between cycles. The sonicates are centrifuged in a Sorvall SS34 rotor at 6000 RPM for 10 minutes. The resultant supernatants are filtered through a 0.2 µ filter. The 3 ml fractions of the filtrates are applied to Bio-Rad Econo-Pac 10DG columns that have been previously equilibrated with 10 ml of 50mM NaCl, 25 mM Tris base, pH 7.0. The flow through collected during sample loading is discarded. The samples are fractionated with two subsequent additions of 4 ml each of the NaCl - Tris equilibration buffer. The two four ml fractions are saved for testing. The first fraction contains all material above about 6,000 mol. wt; the second fraction contains material smaller than 6,000 mol. wt. A sample of the whole culture broth, the sonicate, and the filtered supernatant on the sonicate are tested along with the three fractions from the 10DG column for activity on *P. xylostella* neonates in bioassays.

The culture, the sonicate, and the filtered supernatant of the sonicate, and the first column fraction from the 9359-7 sample are highly active on *P. xylostella*. The second column fraction from 9359-7 is slightly active (some stunting only). No activity is found in the third fraction from 9359-7. The sample from DH5-pUC19 does not have any activity. This indicates that the molecular weights of the toxins are above 6,000.

Example 10: Heat Inactivitation of pCIB9359-7 Activity

The heat stability of the toxins is determined. Overnight cultures of the *E. coli* strain pCIB9359-7 are grown in a 50:50 mixture of Luria broth and Terrific broth. Cultures are grown at 37°C in culture tubes on a tube roller. A one ml sample of the culture is placed in

a 1.5 ml eppendorf tube and placed in a boiling water bath. The sample is removed after five minutes and allowed to cool to room temperature. This sample along with an untreated portion of the culture is assayed on *P. xylostella*. 50µl of sample of sample is spread on diet, allowed to dry and neonate larvae *P. xylostella* applied to the surface. The assay is incubated for 5 days at room temperature.

The untreated sample causes 100% mortality. The heat treated sample and a diet alone control do not cause any observable mortality, showing the toxins are heat sensitive.

Example 11: Leaf Dip Bioassay of pCIB9359-7

Insecticidal activity of the toxins is tested in a leaf dip bioassay. Six leaves approximately 2cm in diameter each are cut from seedlings of turnip and placed in a 1oz. plastic cup (Jet Plastica) with 4ml-5ml of the resuspended toxin, covered tightly, and shaken until thoroughly wetted. The treated leaves are placed in 50mm petri dishes (Gelman Sciences) on absorbent pads moistened with 300µl of water. The dish covers are left open until the leaf surface appears dry and then placed on tightly so that the leaves do not dry out.

Ten neonate *P. xylostella* larvae are placed in each petri dish arena. Also, a treatment of 0.1% Bond spreader/sticker with no toxin is set up as a control. The arenas are monitored daily for signs of drying leaves, and water is added or leaves replaced if necessary. After 3 days the leaves and arenas are examined under a dissecting microscope, and the number of live larvae in each arena is recorded.

100% mortality is found for 9359-7 and none in the no-toxin control, showing that the toxins are also insecticidal in a leaf dip assay.

B. Isolation Of Nucleic Acid Sequences Whose Expression Results In Toxins Active Against Lepidopteran and Coleopteran Insects

Example 12: Total DNA Isolation from *Photorhabdus luminescens*

Photorhabdus luminescens strain ATCC 29999 is grown 14-18 hours in L broth. Total DNA is isolated from 1.5 mls of culture resuspended in 0.5% SDS, 100µg/ml proteinase K, TE to a final volume of 600 µl. After a 1 hour incubation at 37°C, 100µl 5M

NaCl and 80µl CTAB/NaCl are added and the culture is incubated at 65°C for 10 minutes. An equal volume of chloroform is added; the culture is mixed gently and spun. The aqueous phase is extracted once with phenol and once with chloroform. The nucleic acids are treated with 10 µg RNase A for 30 minutes at room temperature. The aqueous phase is mixed with 0.6 volumes isopropanol and the sample is centrifuged. The pellet is washed once with 70% ethanol and the nucleic acids are gently resuspended in 100-200ul TE.

Example 13: PCR Amplification of Probes

Two probes are PCR amplified from *Photorhabdus luminescens* strain ATCC 29999 genomic DNA using oligos 5'-ACACAGCAGGTTCGTCAG-3' (SEQ ID NO:7) and 5'-GGCAGAAGCACTCAACTC-3' (SEQ ID NO:8) to amplify probe #1 and oligos 5'-ATTGATAGCACGCGGCGACC-3' (SEQ ID NO:9) and 5'-TTGTAACGTGGAGCCGAACTGG-3' (SEQ ID NO:10) to amplify probe #2. The oligos are ordered from Genosys Biotechnologies, Inc. (Texas). Approximately 10-50 ng of genomic DNA is used as the template. 0.8µM of oligos, 200µM of dNTPs, 1X Taq DNA Polymerase buffer and 2.5 units of Taq DNA Polymerase are included in the reaction. The reaction conditions are as follows:

94°C - 1 minute

94°C - 30 seconds / 60°C - 30 seconds / 72°C - 30 seconds (25 cycles)

72°C - 5 minutes

4°C - indefinite soak

The reactions are preferably carried out in a PCR System 9600 (Perkin Elmer) thermocycler.

Example 14: Probing a *Photorhabdus luminescens* Library

600 clones from the *P. luminescens* cosmid library described in Example 1 are patched to L-amp plates in duplicate. The colonies are grown overnight then moved to 4°C. The colonies are lifted onto Colony/Plaque Screen Hybridization Transfer Membranes (Biotechnology Systems NEN Research Products). The membranes are incubated 2-3 minutes in 0.75ml 0.5N NaOH twice. The membranes are then incubated 2-3 minutes in

0.75ml 1.0M Tris-HCl, pH 7.5 twice. The membranes are allowed to dry at room temperature.

Probe #1 and probe #2 described in Example 13 are labeled using the DECAprime II Kit as described by the manufacturer (Ambion cat# 1455). Unincorporated nucleotides are removed from the labeled probes using Quick Spin Columns as described by the manufacturer (Boehringer Mannheim cat #1273973). The labeled probes are measured for incorporated radioactivity and the specific activity is 10,000,000 cpm. Membranes are prewetted with 2X SSC and hybridized with the probes for 12-16 hours at 65°C. One set of colony lifts is hybridized with probe #1 and the other set is hybridized with probe #2. The membranes are washed with wash CHURCH solutions 1 and 2 (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1984)) and exposed to Kodak film.

Twenty one clones are identified that hybridize to probe #1 and seven clones are identified that hybridize to probe #2. The gene in the clones isolated with probe #1 is named *hph1* and the gene in the clones isolated with probe #2 is named *hph2*.

Example 15: Insect Bioassays

The clones identified in Example 14 are tested for insecticidal activity against the following insects in insect bioassays: *Diabrotica virgifera virgifera* (Western Corn Rootworm (WCR)), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm (SCR)), *Ostrinia nubilalis* (European Corn Borer (ECB)), and *Plutella xylostella* (Diamondback Moth (DBM)).

Diabrotica virgifera virgifera (Western Corn Rootworm) and *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm) assays are performed using a diet incorporation method. 500µl of an overnight culture of the cosmid library in XL-1 Blue MR cells (Stratagene) is sonicated and then mixed with 500µl of diet. Once the diet solidifies, it is dispensed in a petri dish and 20 larvae are introduced over the diet. Trays of dishes are placed in an incubator for 3-5 days, and percent mortality is recorded at the end of the assay period.

Ostrinia nubilalis (European Corn Borer) and *Plutella xylostella* (Diamondback Moth) assays are performed by a surface treatment method. The diet is poured in the petri dish and allowed it to solidify. The *E. coli* culture of 200 -300µl volume is dispensed over the diet surface and entire diet surface is covered to spread the culture with the help of bacterial loop. Once the surface is dry, 10 larvae are introduced over the diet surface. Trays of

dishes are placed in an incubator for 3-5 days. The assay with European Corn Borer is incubated at 30°C in complete darkness; the assay with Diamondback Moth is incubated at 72°F with a 14:10 (hours) light:dark cycle. Percent mortality is recorded at the end of the assay period.

Cosmids containing *hph2* are identified with a range of activities, including: WCR only; SCR only; WCR and SCR; SCR and ECB; WCR, SCR, and ECB; or WCR, SCR, ECB, and DBM activity.

In addition to probing the *P. luminescens* cosmid library with DNA probes, 600 clones are screened by Western Corn Rootworm bioassay. A clone is identified with activity against Western Corn Rootworm. This clone hybridizes with probe #2.

From these bioassays, cosmid 514, having activity against WCR, SCR, ECB, and DBM, is selected for sequencing.

Example 16: Sequencing of Cosmid 514

Cosmid 514 is sequenced using dye terminator chemistry on an ABI 377 instrument. The nucleotide sequence of cosmid 514 is set forth as SEQ ID NO:11. Cosmid 514 is designated pNOV2400 and deposited with the NRRL in *E. coli* DH5α and assigned accession no. B-30077.

Example 17: Subcloning Insecticidal Regions of Cosmid 514

514a

An 9011 base pair fragment within cosmid 514 (SEQ ID NO:11) is removed by digesting the cosmid with the restriction endonuclease *Spe*I (New England Biolabs (Massachusetts), and ligating (T4 DNA Ligase, NEB) the remainder of 514. Subclone 514a consists of cosmid 514 DNA from base pairs 1-2157 ligated to base pairs 11,169-37,948.

H2O2/pET34

hph2 and *orf2* (SEQ ID NO:11, base pairs 23,768-35,838) are cloned into pET34b (Novagen, Wisconsin). Restriction sites are engineered on both ends of each gene to facilitate cloning. PCR is used to add the restriction sites to the genes. A *Bam*HI site is on the 5' end of *hph2* immediately upstream of the ATG of *hph2*, and a *Sac*I site is added to

the 3' end of *hph2* immediately following the DNA triplet encoding the stop codon. A guanidine is added between the *Bam*HI site and the start codon of *hph2* to put the *hph2* gene in frame with the Cellulose Binding Domain tag in pET34b. *Orf2* has a *Sac*I site upstream of the 56 base pairs between the stop codon of *hph2* and the start codon of *orf2*. The 56 base pairs are included in the *hph2-orf2* construct to mimic their setup in the 514 cosmid. *Orf2* has an *Xho*I site on the 3' end immediately following the stop codon. The oligos used to add the restriction sites to *hph2* and *orf2* are as follows:

hph2-A	5'-CGGGATCCGATGATTTTAAAAGG-3' (SEQ ID NO:15)
hph2-B	5'-GCGCCATTGATTTGAG-3' (SEQ ID NO:16)
hph2-C	5'-CATTAGAGGTCGAACGTAC-3' (SEQ ID NO:17)
hph2-D	5'-GAGCGAGCTCTTACTTAATGGTGTAG-3' (SEQ ID NO:18)
orf2-A3	5'-CAGCGAGCTCCATGCAGAATTCACAGAC-3' (SEQ ID NO:19)
orf2-B	5'-GGCAATGGCAGCGATAAG-3' (SEQ ID NO:20)
orf2-C	5'-CATTAACGCAGGAAGAGC-3' (SEQ ID NO:21)
orf2-D	5'-GACCTCGAGTTACACGAGCGCGTCAG-3' (SEQ ID NO:22)

The *Bam*HI-*Sac*I 7583 base pair fragment, corresponding to the *hph2* gene, and the *Sac*I-*Xho*I 4502 base pair *orf2* (including the 56 base pairs between *hph2* and *orf2* open reading frames), corresponding to *orf2*, are ligated with *Bam*HI-*Xho*I-digested vector DNA pET34b.

Orf5/pBS (*Not*I-*Bam*HI)

The 5325 base pair *Not*I-*Bam*HI fragment of cosmid 514 is cloned into pBS-SK using *Afl*II-*Not*I (415 bp) and *Bam*HI-*Afl*II (2530 bp) fragments of pBS-SK.

O5-H2-O2

The 12,031 base pair *Bam*HI-*Xho*I fragment of H2O2/pET34 is cloned into the 8220 base pair *Xho*I-*Bam*HI fragment of Orf5/pBS.

O51011H2O2

A 7298 base pair *Bam*HI-*Mlu*I fragment from subclone 514a is ligated (T4 DNA Ligase, NEB) with 9588 bp *Mlu*I-*Xho*I and 8220 bp *Xho*I-*Bam*HI fragments of subclone O5-H2-O2. The resulting ~ 22 kb subclone O51011H2O2, which has activity against WCR and

ECB, is designated pNOV1001 and deposited with the NRRL in *E. coli* DH5α and assigned accession no. B-30078.

AKH2O2

A 12,074 base pair *Bam*HI-*Avr*II fragment of H2O2/pET34 is ligated (T4 DNA Ligase, NEB) into pK184 *Nhe*I-*Bam*HI fragment (2228 bp), generating a clone containing hph2 and orf2 in a p15a origin of replication, kanamycin-resistant vector.

Example 18: Insecticidal Activity of Subclones

Bioassays as described above are performed with *E. coli* cultures that express the above subclones, both singly and in combination. Coexpressing AKH2O2 and Orf5/pBS in *E. coli*, for example in DH5α or HB101, is found to give insecticidal activity against the Lepidopterans *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), as well as against the Coleopterans *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle). Thus, coexpression of hph2 (SEQ ID NO:11, base pairs 23,768-31,336), orf2 (SEQ ID NO:11, base pairs 31,393-35,838), and orf5 (SEQ ID NO:11, base pairs 15,171-18,035) is sufficient to control these insects. In addition, expression of each of these three ORFs on separate plasmids gives insect control activity, demonstrating that they do not have to be genetically linked to be active, so long as all three gene products are present.

C. Expression of the Nucleic Acid Sequences of the Invention in Heterologous Microbial Hosts

Microorganisms which are suitable for the heterologous expression of the nucleotide sequences of the invention are all microorganisms which are capable of colonizing plants or the rhizosphere. As such they will be brought into contact with insect pests. These include gram-negative microorganisms such as *Pseudomonas, Enterobacter* and *Serratia*, the gram-positive microorganism *Bacillus* and the fungi *Trichoderma*, *Gliocladium*, and *Saccharomyces cerevisiae*. Particularly preferred heterologous hosts are *Pseudomonas fluorescens, Pseudomonas putida, Pseudomonas cepacia, Pseudomonas aureofaciens,*

Pseudomonas aurantiaca, Enterobacter cloacae, Serratia marscesens, Bacillus subtilis, Bacillus cereus, Trichoderma viride, Trichoderma harzianum, Gliocladium virens, and *Saccharomyces cerevisiae.*

Example 19: Expression of the Nucleotide Sequences in *E. coli* and Other Gram-Negative Bacteria

Many genes have been expressed in gram-negative bacteria in a heterologous manner. Expression vector pKK223-3 (Pharmacia catalogue # 27-4935-01) allows expression in *E. coli.* This vector has a strong *tac* promoter (Brosius, J. *et al., Proc. Natl. Acad. Sci. USA 81)* regulated by the *lac* repressor and induced by IPTG. A number of other expression systems have been developed for use in *E. coli.* The thermoinducible expression vector pP_L (Pharmacia #27-4946-01) uses a tightly regulated bacteriophage λ promoter which allows for high level expression of proteins. The *lac* promoter provides another means of expression but the promoter is not expressed at such high levels as the *tac* promoter. With the addition of broad host range replicons to some of these expression system vectors, expression of the nucleotide sequence in closely related gram negative-bacteria such as *Pseudomonas*, *Enterobacter*, *Serratia* and *Erwinia* is possible. For example, pLRKD211 (Kaiser & Kroos, Proc. Natl. Acad. Sci. USA 81: 5816-5820 (1984)) contains the broad host range replicon *ori T* which allows replication in many gram-negative bacteria.

In *E. coli*, induction by IPTG is required for expression of the *tac* (*i.e. trp-lac*) promoter. When this same promoter (*e.g.* on wide-host range plasmid pLRKD211) is introduced into *Pseudomonas* it is constitutively active without induction by IPTG. This *trp-lac* promoter can be placed in front of any gene or operon of interest for expression in *Pseudomonas* or any other closely related bacterium for the purposes of the constitutive expression of such a gene. Thus, a nucleotide sequence whose expression results in an insecticidal toxin can therefore be placed behind a strong constitutive promoter, transferred to a bacterium which has plant or rhizosphere colonizing properties turning this organism to an insecticidal agent. Other possible promoters can be used for the constitutive expression of the nucleotide sequence in gram-negative bacteria. These include, for example, the promoter from the *Pseudomonas* regulatory genes *gafA* and *lemA* (WO 94/01561) and the

Pseudomonas savastanoi IAA operon promoter (Gaffney *et al., J. Bacteriol. 172:* 5593-5601 (1990).

Example 20: Expression of the Nucleotide Sequences in Gram-Positive Bacteria

Heterologous expression of the nucleotides sequence in gram-positive bacteria is another means of producing the insecticidal toxins. Expression systems for *Bacillus* and *Streptomyces* are the best characterized. The promoter for the erythromycin resistance gene (*ermR*) from *Streptococcus pneumoniae* has been shown to be active in gram-positive aerobes and anaerobes and also in *E.coli* (Trieu-Cuot *et al.*, Nucl Acids Res 18: 3660 (1990)). A further antibiotic resistance promoter from the thiostreptone gene has been used in *Streptomyces* cloning vectors (Bibb, Mol Gen Genet 199: 26-36 (1985)). The shuttle vector pHT3101 is also appropriate for expression in *Bacillus* (Lereclus, FEMS Microbiol Lett 60: 211-218 (1989)). A significant advantage of this approach is that many gram-positive bacteria produce spores which can be used in formulations that produce insecticidal agents with a longer shelf life. *Bacillus* and *Streptomyces* species are aggressive colonizers of soils

Example 21: Expression of the Nucleotide Sequences in Fungi

Trichoderma harzianum and *Gliocladium virens* have been shown to provide varying levels of biocontrol in the field (US 5,165,928 and US 4,996,157, both to Cornell Research Foundation). A nucleotide sequence whose expression results in an insecticidal toxin could be expressed in such a fungus. This could be accomplished by a number of ways which are well known in the art. One is protoplast-mediated transformation of the fungus by PEG or electroporation-mediated techniques. Alternatively, particle bombardment can be used to transform protoplasts or other fungal cells with the ability to develop into regenerated mature structures. The vector pAN7-1, originally developed for *Aspergillus* transformation and now used widely for fungal transformation (Curragh *et al., Mycol. Res. 97(3):* 313-317 (1992); Tooley *et al., Curr. Genet. 21:* 55-60 (1992); Punt *et al.*, Gene 56: 117-124 (1987)) is engineered to contain the nucleotide sequence. This plasmid contains the *E. coli* the hygromycin B resistance gene flanked by the *Aspergillus nidulans gpd* promoter and the *trpC* terminator (Punt *et al.*, Gene 56: 117-124 (1987)).

In a preferred embodiment, the nucleic acid sequences of the invention are expressed in the yeast *Saccharomyces cerevisiae*. Each of the three ORF's of SEQ ID NO:11 (hph2, orf2 and orf5), which together confer insecticidal activity, are cloned into individual vectors with the GAL1 inducible promoter and the CYC1 terminator. Each vector has ampicillin resistance and the 2 micron replicon. The vectors differ in their yeast growth markers. hph2 is cloned into p424 (TRP1, ATCC 87329), orf2 into p423 (HIS3, ATCC 87327), and orf5 into p425 (LEU2, ATCC 87331). The three constructs are transformed into *S. cerevisiae* independently and together. The three ORFs are expressed together and tested for protein expression and insecticidal activity.

D. Expression of the Nucleotide Sequences in Transgenic Plants

The nucleic acid sequences described in this application can be incorporated into plant cells using conventional recombinant DNA technology. Generally, this involves inserting a coding sequence of the invention into an expression system to which the coding sequence is heterologous (i.e., not normally present) using standard cloning procedures known in the art. The vector contains the necessary elements for the transcription and translation of the inserted protein-coding sequences. A large number of vector systems known in the art can be used, such as plasmids, bacteriophage viruses and other modified viruses. Suitable vectors include, but are not limited to, viral vectors such as lambda vector systems λgtl1, λgtl0 and Charon 4; plasmid vectors such as pBI121, pBR322, pACYC177, pACYC184, pAR series, pKK223-3, pUC8, pUC9, pUC18, pUC19, pLG339, pRK290, pKC37, pKC101, pCDNAII; and other similar systems. The components of the expression system may also be modified to increase expression. For example, truncated sequences, nucleotide substitutions or other modifications may be employed. The expression systems described herein can be used to transform virtually any crop plant cell under suitable conditions. Transformed cells can be regenerated into whole plants such that the nucleotide sequence of the invention confer insect resistance to the transgenic plants.

Example 22: Modification of Coding Sequences and Adjacent Sequences

The nucleotide sequences described in this application can be modified for expression in transgenic plant hosts. A host plant expressing the nucleotide sequences and

which produces the insecticidal toxins in its cells has enhanced resistance to insect attack and is thus better equipped to withstand crop losses associated with such attack.

The transgenic expression in plants of genes derived from microbial sources may require the modification of those genes to achieve and optimize their expression in plants. In particular, bacterial ORFs which encode separate enzymes but which are encoded by the same transcript in the native microbe are best expressed in plants on separate transcripts. To achieve this, each microbial ORF is isolated individually and cloned within a cassette which provides a plant promoter sequence at the 5' end of the ORF and a plant transcriptional terminator at the 3' end of the ORF. The isolated ORF sequence preferably includes the initiating ATG codon and the terminating STOP codon but may include additional sequence beyond the initiating ATG and the STOP codon. In addition, the ORF may be truncated, but still retain the required activity; for particularly long ORFs, truncated versions which retain activity may be preferable for expression in transgenic organisms. By "plant promoter" and "plant transcriptional terminator" it is intended to mean promoters and transcriptional terminators which operate within plant cells. This includes promoters and transcription terminators which may be derived from non-plant sources such as viruses (an example is the Cauliflower Mosaic Virus).

In some cases, modification to the ORF coding sequences and adjacent sequence is not required. It is sufficient to isolate a fragment containing the ORF of interest and to insert it downstream of a plant promoter. For example, Gaffney *et al.* (Science 261: 754-756 (1993)) have expressed the *Pseudomonas nahG* gene in transgenic plants under the control of the CaMV 35S promoter and the CaMV *tml* terminator successfully without modification of the coding sequence and with x bp of the *Pseudomonas* gene upstream of the ATG still attached, and y bp downstream of the STOP codon still attached to the *nahG* ORF. Preferably as little adjacent microbial sequence should be left attached upstream of the ATG and downstream of the STOP codon. In practice, such construction may depend on the availability of restriction sites.

In other cases, the expression of genes derived from microbial sources may provide problems in expression. These problems have been well characterized in the art and are particularly common with genes derived from certain sources such as *Bacillus*. These problems may apply to the nucleotide sequence of this invention and the modification of these genes can be undertaken using techniques now well known in the art. The following problems may be encountered:

1. Codon Usage.

The preferred codon usage in plants differs from the preferred codon usage in certain microorganisms. Comparison of the usage of codons within a cloned microbial ORF to usage in plant genes (and in particular genes from the target plant) will enable an identification of the codons within the ORF which should preferably be changed. Typically plant evolution has tended towards a strong preference of the nucleotides C and G in the third base position of monocotyledons, whereas dicotyledons often use the nucleotides A or T at this position. By modifying a gene to incorporate preferred codon usage for a particular target transgenic species, many of the problems described below for GC/AT content and illegitimate splicing will be overcome.

2. GC/AT Content.

Plant genes typically have a GC content of more than 35%. ORF sequences which are rich in A and T nucleotides can cause several problems in plants. Firstly, motifs of ATTTA are believed to cause destabilization of messages and are found at the 3' end of many short-lived mRNAs. Secondly, the occurrence of polyadenylation signals such as AATAAA at inappropriate positions within the message is believed to cause premature truncation of transcription. In addition, monocotyledons may recognize AT-rich sequences as splice sites (see below).

3. Sequences Adjacent to the Initiating Methionine.

Plants differ from microorganisms in that their messages do not possess a defined ribosome binding site. Rather, it is believed that ribosomes attach to the 5' end of the message and scan for the first available ATG at which to start translation. Nevertheless, it is believed that there is a preference for certain nucleotides adjacent to the ATG and that expression of microbial genes can be enhanced by the inclusion of a eukaryotic consensus translation initiator at the ATG. Clontech (1993/1994 catalog, page 210, incorporated herein by reference) have suggested one sequence as a consensus translation initiator for the expression of the *E. coli uidA* gene in plants. Further, Joshi (NAR 15: 6643-6653 (1987), incorporated herein by reference) has compared many plant sequences adjacent to the ATG and suggests another consensus sequence. In situations where difficulties are encountered in the expression of microbial ORFs in plants, inclusion of one of these sequences at the initiating ATG may improve translation. In such cases the last three

nucleotides of the consensus may not be appropriate for inclusion in the modified sequence due to their modification of the second AA residue. Preferred sequences adjacent to the initiating methionine may differ between different plant species. A survey of 14 maize genes located in the GenBank database provided the following results:

Position Before the Initiating ATG in 14 Maize Genes:

	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1
C	3	8	4	6	2	5	6	0	10	7
T	3	0	3	4	3	2	1	1	1	0
A	2	3	1	4	3	2	3	7	2	3
G	6	3	6	0	6	5	4	6	1	5

This analysis can be done for the desired plant species into which the nucleotide sequence is being incorporated, and the sequence adjacent to the ATG modified to incorporate the preferred nucleotides.

4. Removal of Illegitimate Splice Sites.

Genes cloned from non-plant sources and not optimized for expression in plants may also contain motifs which may be recognized in plants as 5' or 3' splice sites, and be cleaved, thus generating truncated or deleted messages. These sites can be removed using the techniques well known in the art.

Techniques for the modification of coding sequences and adjacent sequences are well known in the art. In cases where the initial expression of a microbial ORF is low and it is deemed appropriate to make alterations to the sequence as described above, then the construction of synthetic genes can be accomplished according to methods well known in the art. These are, for example, described in the published patent disclosures EP 0 385 962 (to Monsanto), EP 0 359 472 (to Lubrizol) and WO 93/07278 (to Ciba-Geigy), all of which are incorporated herein by reference. In most cases it is preferable to assay the expression of gene constructions using transient assay protocols (which are well known in the art) prior to their transfer to transgenic plants.

Example 23: Construction of Plant Expr ssion Cass tt s

Coding sequences intended for expression in transgenic plants are first assembled in expression cassettes behind a suitable promoter expressible in plants. The expression cassettes may also comprise any further sequences required or selected for the expression of the transgene. Such sequences include, but are not restricted to, transcription terminators, extraneous sequences to enhance expression such as introns, vital sequences, and sequences intended for the targeting of the gene product to specific organelles and cell compartments. These expression cassettes can then be easily transferred to the plant transformation vectors described below. The following is a description of various components of typical expression cassettes.

1. Promoters

The selection of the promoter used in expression cassettes will determine the spatial and temporal expression pattern of the transgene in the transgenic plant. Selected promoters will express transgenes in specific cell types (such as leaf epidermal cells, mesophyll cells, root cortex cells) or in specific tissues or organs (roots, leaves or flowers, for example) and the selection will reflect the desired location of accumulation of the gene product. Alternatively, the selected promoter may drive expression of the gene under various inducing conditions. Promoters vary in their strength, i.e., ability to promote transcription. Depending upon the host cell system utilized, any one of a number of suitable promoters can be used, including the gene's native promoter. The following are non-limiting examples of promoters that may be used in expression cassettes.

a. Constitutive Expression, the Ubiquitin Promoter:

Ubiquitin is a gene product known to accumulate in many cell types and its promoter has been cloned from several species for use in transgenic plants (*e.g.* sunflower - Binet *et al.* Plant Science 79: 87-94 (1991); maize - Christensen *et al.* Plant Molec. Biol. 12: 619-632 (1989); and *Arabidopsis* - Norris *et al.*, *Plant Mol. Biol.* 21:895-906 (1993)). The maize ubiquitin promoter has been developed in transgenic monocot systems and its sequence and vectors constructed for monocot transformation are disclosed in the patent publication EP 0 342 926 (to Lubrizol) which is herein incorporated by reference. Taylor *et al.* (Plant Cell Rep. 12: 491-495 (1993)) describe a vector (pAHC25) that comprises the maize ubiquitin promoter and first intron and its high activity in cell suspensions of numerous

monocotyledons when introduced via microprojectile bombardment. The *Arabidopsis* ubiquitin promoter is ideal for use with the nucleotide sequences of the present invention. The ubiquitin promoter is suitable for gene expression in transgenic plants, both monocotyledons and dicotyledons. Suitable vectors are derivatives of pAHC25 or any of the transformation vectors described in this application, modified by the introduction of the appropriate ubiquitin promoter and/or intron sequences.

b. Constitutive Expression, the CaMV 35S Promoter:

Construction of the plasmid pCGN1761 is described in the published patent application EP 0 392 225 (Example 23), which is hereby incorporated by reference. pCGN1761 contains the "double" CaMV 35S promoter and the *tml* transcriptional terminator with a unique *EcoRI* site between the promoter and the terminator and has a pUC-type backbone. A derivative of pCGN1761 is constructed which has a modified polylinker which includes *NotI* and *XhoI* sites in addition to the existing *EcoRI* site. This derivative is designated pCGN1761ENX. pCGN1761ENX is useful for the cloning of cDNA sequences or coding sequences (including microbial ORF sequences) within its polylinker for the purpose of their expression under the control of the 35S promoter in transgenic plants. The entire 35S promoter-coding sequence-*tml* terminator cassette of such a construction can be excised by *HindIII, SphI, SalI,* and *XbaI* sites 5' to the promoter and *XbaI, BamHI* and *BglI* sites 3' to the terminator for transfer to transformation vectors such as those described below. Furthermore, the double 35S promoter fragment can be removed by 5' excision with *HindIII, SphI, SalI, XbaI*, or *PstI*, and 3' excision with any of the polylinker restriction sites (*EcoRI, NotI* or *XhoI*) for replacement with another promoter. If desired, modifications around the cloning sites can be made by the introduction of sequences that may enhance translation. This is particularly useful when overexpression is desired. For example, pCGN1761ENX may be modified by optimization of the translational initiation site as described in Example 37 of U.S. Patent No. 5,639,949, incorporated herein by reference.

c. Constitutive Expression, the Actin Promoter:

Several isoforms of actin are known to be expressed in most cell types and consequently the actin promoter is a good choice for a constitutive promoter. In particular, the promoter from the rice *Act1* gene has been cloned and characterized (McElroy *et al.* Plant Cell 2: 163-171 (1990)). A 1.3kb fragment of the promoter was found to contain all

the regulatory elements required for expression in rice protoplasts. Furthermore, numerous expression vectors based on the *Actl* promoter have been constructed specifically for use in monocotyledons (McElroy *et al.* Mol. Gen. Genet. 231: 150-160 (1991)). These incorporate the *Actl*-intron 1, *Adhl* 5' flanking sequence and *Adhl*-intron 1 (from the maize alcohol dehydrogenase gene) and sequence from the CaMV 35S promoter. Vectors showing highest expression were fusions of 35S and *Actl* intron or the *Actl* 5' flanking sequence and the *Actl* intron. Optimization of sequences around the initiating ATG (of the GUS reporter gene) also enhanced expression. The promoter expression cassettes described by McElroy *et al.* (Mol. Gen. Genet. 231: 150-160 (1991)) can be easily modified for gene expression and are particularly suitable for use in monocotyledonous hosts. For example, promoter-containing fragments is removed from the McElroy constructions and used to replace the double 35S promoter in pCGN1761ENX, which is then available for the insertion of specific gene sequences. The fusion genes thus constructed can then be transferred to appropriate transformation vectors. In a separate report, the rice *Actl* promoter with its first intron has also been found to direct high expression in cultured barley cells (Chibbar *et al.* Plant Cell Rep. 12: 506-509 (1993)).

d. Inducible Expression, the PR-1 Promoter:

The double 35S promoter in pCGN1761ENX may be replaced with any other promoter of choice that will result in suitably high expression levels. By way of example, one of the chemically regulatable promoters described in U.S. Patent No. 5,614,395 may replace the double 35S promoter. The promoter of choice is preferably excised from its source by restriction enzymes, but can alternatively be PCR-amplified using primers that carry appropriate terminal restriction sites. Should PCR-amplification be undertaken, then the promoter should be re-sequenced to check for amplification errors after the cloning of the amplified promoter in the target vector. The chemically/pathogen regulatable tobacco PR-1a promoter is cleaved from plasmid pCIB1004 (for construction, see example 21 of EP 0 332 104, which is hereby incorporated by reference) and transferred to plasmid pCGN1761ENX (Uknes et al., 1992). pCIB1004 is cleaved with *NcoI* and the resultant 3' overhang of the linearized fragment is rendered blunt by treatment with T4 DNA polymerase. The fragment is then cleaved with *HindIII* and the resultant PR-1a promoter-containing fragment is gel purified and cloned into pCGN1761ENX from which the double 35S promoter has been removed. This is done by cleavage with *XhoI* and blunting with T4

polymerase, followed by cleavage with *HindIII* and isolation of the larger vector-terminator containing fragment into which the pCIB1004 promoter fragment is cloned. This generates a pCGN1761ENX derivative with the PR-1a promoter and the *tml* terminator and an intervening polylinker with unique *EcoRI* and *NotI* sites. The selected coding sequence can be inserted into this vector, and the fusion products (*i.e.* promoter-gene-terminator) can subsequently be transferred to any selected transformation vector, including those described *infra*. Various chemical regulators may be employed to induce expression of the selected coding sequence in the plants transformed according to the present invention, including the benzothiadiazole, isonicotinic acid, and salicylic acid compounds disclosed in U.S. Patent Nos. 5,523,311 and 5,614,395.

e. Inducible Expression, an Ethanol-Inducible Promoter:

A promoter inducible by certain alcohols or ketones, such as ethanol, may also be used to confer inducible expression of a coding sequence of the present invention. Such a promoter is for example the *alcA* gene promoter from *Aspergillus nidulans* (Caddick et al. (1998) *Nat. Biotechnol* 16:177-180). In *A. nidulans*, the *alcA* gene encodes alcohol dehydrogenase I, the expression of which is regulated by the AlcR transcription factors in presence of the chemical inducer. For the purposes of the present invention, the CAT coding sequences in plasmid palcA:CAT comprising a *alcA* gene promoter sequence fused to a minimal 35S promoter (Caddick et al. (1998) *Nat. Biotechnol* 16:177-180) are replaced by a coding sequence of the present invention to form an expression cassette having the coding sequence under the control of the *alcA* gene promoter. This is carried out using methods well known in the art.

f. Inducible Expression, a Glucocorticoid-Inducible Promoter:

Induction of expression of a nucleic acid sequence of the present invention using systems based on steroid hormones is also contemplated. For example, a glucocorticoid-mediated induction system is used (Aoyama and Chua (1997) *The Plant Journal* 11: 605-612) and gene expression is induced by application of a glucocorticoid, for example a synthetic glucocorticoid, preferably dexamethasone, preferably at a concentration ranging from 0.1mM to 1mM, more preferably from 10mM to 100mM. For the purposes of the present invention, the luciferase gene sequences are replaced by a nucleic acid sequence of the invention to form an expression cassette having a nucleic acid sequence of the

invention under the control of six copies of the GAL4 upstream activating sequences fused to the 35S minimal promoter. This is carried out using methods well known in the art. The trans-acting factor comprises the GAL4 DNA-binding domain (Keegan et al. (1986) *Science* 231: 699-704) fused to the transactivating domain of the herpes viral protein VP16 (Triezenberg et al. (1988) *Genes Devel.* 2: 718-729) fused to the hormone-binding domain of the rat glucocorticoid receptor (Picard et al. (1988) *Cell* 54: 1073-1080). The expression of the fusion protein is controlled by any promoter suitable for expression in plants known in the art or described here. This expression cassette is also comprised in the plant comprising a nucleic acid sequence of the invention fused to the 6xGAL4/minimal promoter. Thus, tissue- or organ-specificity of the fusion protein is achieved leading to inducible tissue- or organ-specificity of the insecticidal toxin.

g. Root Specific Expression:

Another pattern of gene expression is root expression. A suitable root promoter is described by de Framond (FEBS 290: 103-106 (1991)) and also in the published patent application EP 0 452 269, which is herein incorporated by reference. This promoter is transferred to a suitable vector such as pCGN1761ENX for the insertion of a selected gene and subsequent transfer of the entire promoter-gene-terminator cassette to a transformation vector of interest.

h. Wound-Inducible Promoters:

Wound-inducible promoters may also be suitable for gene expression. Numerous such promoters have been described (*e.g.* Xu *et al.* Plant Molec. Biol. 22: 573-588 (1993), Logemann *et al.* Plant Cell 1: 151-158 (1989), Rohrmeier & Lehle, Plant Molec. Biol. 22: 783-792 (1993), Firek *et al.* Plant Molec. Biol. 22: 129-142 (1993), Warner *et al.* Plant J. 3: 191-201 (1993)) and all are suitable for use with the instant invention. Logemann *et al.* describe the 5' upstream sequences of the dicotyledonous potato *wun1* gene. Xu *et al.* show that a wound-inducible promoter from the dicotyledon potato (*pin2*) is active in the monocotyledon rice. Further, Rohrmeier & Lehle describe the cloning of the maize *Wip1* cDNA which is wound induced and which can be used to isolate the cognate promoter using standard techniques. Similar, Firek *et al.* and Warner *et al.* have described a wound-induced gene from the monocotyledon *Asparagus officinalis,* which is expressed at local wound and pathogen invasion sites. Using cloning techniques well known in the art, these

promoters can be transferred to suitable vectors, fused to the genes pertaining to this invention, and used to express these genes at the sites of plant wounding.

i. Pith-Preferred Expression:

Patent Application WO 93/07278, which is herein incorporated by reference, describes the isolation of the maize *trpA* gene, which is preferentially expressed in pith cells. The gene sequence and promoter extending up to -1726 bp from the start of transcription are presented. Using standard molecular biological techniques, this promoter, or parts thereof, can be transferred to a vector such as pCGN1761 where it can replace the 35S promoter and be used to drive the expression of a foreign gene in a pith-preferred manner. In fact, fragments containing the pith-preferred promoter or parts thereof can be transferred to any vector and modified for utility in transgenic plants.

j. Leaf-Specific Expression:

A maize gene encoding phosphoenol carboxylase (PEPC) has been described by Hudspeth & Grula (Plant Molec Biol 12: 579-589 (1989)). Using standard molecular biological techniques the promoter for this gene can be used to drive the expression of any gene in a leaf-specific manner in transgenic plants.

k. Pollen-Specific Expression:

WO 93/07278 describes the isolation of the maize calcium-dependent protein kinase (CDPK) gene which is expressed in pollen cells. The gene sequence and promoter extend up to 1400 bp from the start of transcription. Using standard molecular biological techniques, this promoter or parts thereof, can be transferred to a vector such as pCGN1761 where it can replace the 35S promoter and be used to drive the expression of a nucleic acid sequence of the invention in a pollen-specific manner.

2. Transcriptional Terminators

A variety of transcriptional terminators are available for use in expression cassettes. These are responsible for the termination of transcription beyond the transgene and its correct polyadenylation. Appropriate transcriptional terminators are those that are known to function in plants and include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator and the pea *rbcS* E9 terminator. These can be used in both

monocotyledons and dicotyledons. In addition, a gene's native transcription terminator may be used.

3. Sequences for the Enhancement or Regulation of Expression

Numerous sequences have been found to enhance gene expression from within the transcriptional unit and these sequences can be used in conjunction with the genes of this invention to increase their expression in transgenic plants.

Various intron sequences have been shown to enhance expression, particularly in monocotyledonous cells. For example, the introns of the maize *Adh1* gene have been found to significantly enhance the expression of the wild-type gene under its cognate promoter when introduced into maize cells. Intron 1 was found to be particularly effective and enhanced expression in fusion constructs with the chloramphenicol acetyltransferase gene (Callis *et al.*, Genes Develop. 1: 1183-1200 (1987)). In the same experimental system, the intron from the maize *bronze1* gene had a similar effect in enhancing expression. Intron sequences have been routinely incorporated into plant transformation vectors, typically within the non-translated leader.

A number of non-translated leader sequences derived from viruses are also known to enhance expression, and these are particularly effective in dicotyledonous cells. Specifically, leader sequences from Tobacco Mosaic Virus (TMV, the "W-sequence"), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (*e.g.* Gallie *et al.* Nucl. Acids Res. 15: 8693-8711 (1987); Skuzeski *et al.* Plant Molec. Biol. 15: 65-79 (1990)).

4. Targeting of the Gene Product Within the Cell

Various mechanisms for targeting gene products are known to exist in plants and the sequences controlling the functioning of these mechanisms have been characterized in some detail. For example, the targeting of gene products to the chloroplast is controlled by a signal sequence found at the amino terminal end of various proteins which is cleaved during chloroplast import to yield the mature protein (*e.g.* Comai *et al.* J. Biol. Chem. 263: 15104-15109 (1988)). These signal sequences can be fused to heterologous gene products to effect the import of heterologous products into the chloroplast (van den Broeck, et al. Nature 313: 358-363 (1985)). DNA encoding for appropriate signal sequences can be isolated from the 5' end of the cDNAs encoding the RUBISCO protein, the CAB protein, the

EPSP synthase enzyme, the GS2 protein and many other proteins which are known to be chloroplast localized. *See also*, the section entitled "Expression With Chloroplast Targeting" in Example 37 of U.S. Patent No. 5,639,949.

Other gene products are localized to other organelles such as the mitochondrion and the peroxisome (*e.g.* Unger *et al.* Plant Molec. Biol. 13: 411-418 (1989)). The cDNAs encoding these products can also be manipulated to effect the targeting of heterologous gene products to these organelles. Examples of such sequences are the nuclear-encoded ATPases and specific aspartate amino transferase isoforms for mitochondria. Targeting cellular protein bodies has been described by Rogers *et al.* (Proc. Natl. Acad. Sci. USA 82: 6512-6516 (1985)).

In addition, sequences have been characterized which cause the targeting of gene products to other cell compartments. Amino terminal sequences are responsible for targeting to the ER, the apoplast, and extracellular secretion from aleurone cells (Koehler & Ho, Plant Cell 2: 769-783 (1990)). Additionally, amino terminal sequences in conjunction with carboxy terminal sequences are responsible for vacuolar targeting of gene products (Shinshi *et al.* Plant Molec. Biol. 14: 357-368 (1990)).

By the fusion of the appropriate targeting sequences described above to transgene sequences of interest it is possible to direct the transgene product to any organelle or cell compartment. For chloroplast targeting, for example, the chloroplast signal sequence from the RUBISCO gene, the CAB gene, the EPSP synthase gene, or the GS2 gene is fused in frame to the amino terminal ATG of the transgene. The signal sequence selected should include the known cleavage site, and the fusion constructed should take into account any amino acids after the cleavage site which are required for cleavage. In some cases this requirement may be fulfilled by the addition of a small number of amino acids between the cleavage site and the transgene ATG or, alternatively, replacement of some amino acids within the transgene sequence. Fusions constructed for chloroplast import can be tested for efficacy of chloroplast uptake by *in vitro* translation of *in vitro* transcribed constructions followed by *in vitro* chloroplast uptake using techniques described by Bartlett *et al.* In: Edelmann *et al.* (Eds.) Methods in Chloroplast Molecular Biology, Elsevier pp 1081-1091 (1982) and Wasmann *et al.* Mol. Gen. Genet. 205: 446-453 (1986). These construction techniques are well known in the art and are equally applicable to mitochondria and peroxisomes.

The above-described mechanisms for cellular targeting can be utilized not only in conjunction with their cognate promoters, but also in conjunction with heterologous promoters so as to effect a specific cell-targeting goal under the transcriptional regulation of a promoter that has an expression pattern different to that of the promoter from which the targeting signal derives.

Example 24: Construction of Plant Transformation Vectors

Numerous transformation vectors available for plant transformation are known to those of ordinary skill in the plant transformation arts, and the genes pertinent to this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation. For certain target species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the *nptII* gene, which confers resistance to kanamycin and related antibiotics (Messing & Vierra. Gene 19: 259-268 (1982); Bevan et al., Nature 304:184-187 (1983)), the *bar* gene, which confers resistance to the herbicide phosphinothricin (White et al., Nucl. Acids Res 18: 1062 (1990), Spencer et al. Theor. Appl. Genet 79: 625-631 (1990)), the *hph* gene, which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann, Mol Cell Biol 4: 2929-2931), and the *dhfr* gene, which confers resistance to methatrexate (Bourouis et al., EMBO J. 2(7): 1099-1104 (1983)), and the EPSPS gene, which confers resistance to glyphosate (U.S. Patent Nos. 4,940,935 and 5,188,642).

1. Vectors Suitable for *Agrobacterium* Transformation

Many vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, Nucl. Acids Res. (1984)) and pXYZ. Below, the construction of two typical vectors suitable for *Agrobacterium* transformation is described.

a. pCIB200 and pCIB2001:

The binary vectors pcIB200 and pCIB2001 are used for the construction of recombinant vectors for use with *Agrobacterium* and are constructed in the following manner. pTJS75kan is created by *NarI* digestion of pTJS75 (Schmidhauser & Helinski, J.

Bacteriol. 164: 446-455 (1985)) allowing excision of the tetracycline-resistance gene, followed by insertion of an *AccI* fragment from pUC4K carrying an NPTII (Messing & Vierra, Gene 19: 259-268 (1982): Bevan et al., Nature 304: 184-187 (1983): McBride et al., Plant Molecular Biology 14: 266-276 (1990)). *XhoI* linkers are ligated to the *EcoRV* fragment of PCIB7 which contains the left and right T-DNA borders, a plant selectable *nos/nptII* chimeric gene and the pUC polylinker (Rothstein et al., Gene 53: 153-161 (1987)), and the *XhoI*-digested fragment are cloned into *SalI*-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). pCIB200 contains the following unique polylinker restriction sites: *EcoRI, SstI, KpnI, BglII, XbaI,* and *SalI.* pCIB2001 is a derivative of pCIB200 created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are *EcoRI, SstI, KpnI, BglII, XbaI, SalI, MluI, BclI, AvrII, ApaI, HpaI,* and *StuI.* pCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived *trfA* function for mobilization between *E. coli* and other hosts, and the *OriT* and *OriV* functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

b. pCIB10 and Hygromycin Selection Derivatives thereof:

The binary vector pCIB10 contains a gene encoding kanamycin resistance for selection in plants and T-DNA right and left border sequences and incorporates sequences from the wide host-range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium.* Its construction is described by Rothstein *et al.* (Gene 53: 153-161 (1987)). Various derivatives of pCIB10 are constructed which incorporate the gene for hygromycin B phosphotransferase described by Gritz *et al.* (Gene 25: 179-188 (1983)). These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

2. Vectors Suitable for non-*Agrobacterium* Transformation

Transformation without the use of *Agrobacterium tumefaciens* circumvents the requirement for T-DNA sequences in the chosen transformation vector and consequently vectors lacking these sequences can be utilized in addition to vectors such as the ones described above which contain T-DNA sequences. Transformation techniques that do not rely on *Agrobacterium* include transformation via particle bombardment, protoplast uptake

(*e.g.* PEG and electroporation) and microinjection. The choice of vector depends largely on the preferred selection for the species being transformed. Below, the construction of typical vectors suitable for non-*Agrobacterium* transformation is described.

a. pCIB3064:

pCIB3064 is a pUC-derived vector suitable for direct gene transfer techniques in combination with selection by the herbicide basta (or phosphinothricin). The plasmid pCIB246 comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278. The 35S promoter of this vector contains two ATG sequences 5' of the start site. These sites are mutated using standard PCR techniques in such a way as to remove the ATGs and generate the restriction sites *SspI* and *PvuII*. The new restriction sites are 96 and 37 bp away from the unique *SalI* site and 101 and 42 bp away from the actual start site. The resultant derivative of pCIB246 is designated pCIB3025. The GUS gene is then excised from pCIB3025 by digestion with *SalI* and *SacI*, the termini rendered blunt and religated to generate plasmid pCIB3060. The plasmid pJIT82 is obtained from the John Innes Centre, Norwich and the a 400 bp *SmaI* fragment containing the *bar* gene from *Streptomyces viridochromogenes* is excised and inserted into the *HpaI* site of pCIB3060 (Thompson *et al.* EMBO J 6: 2519-2523 (1987)). This generated pCIB3064, which comprises the *bar* gene under the control of the CaMV 35S promoter and terminator for herbicide selection, a gene for ampicillin resistance (for selection in *E. coli*) and a polylinker with the unique sites *SphI, PstI, HindIII,* and *BamHI*. This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

b. pSOG19 and pSOG35:

pSOG35 is a transformation vector that utilizes the *E. coli* gene dihydrofolate reductase (DFR) as a selectable marker conferring resistance to methotrexate. PCR is used to amplify the 35S promoter (-800 bp), intron 6 from the maize Adh1 gene (-550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250-bp fragment encoding the *E. coli* dihydrofolate reductase type II gene is also amplified by PCR and these two PCR fragments are assembled with a *SacI-PstI* fragment from pB1221 (Clontech) which comprises the pUC19 vector backbone and the nopaline synthase terminator. Assembly of these fragments generates pSOG19 which contains the 35S promoter in fusion

with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus (MCMV) generates the vector pSOG35. pSOG19 and pSOG35 carry the pUC gene for ampicillin resistance and have *HindIII, SphI, PstI* and *EcoRI* sites available for the cloning of foreign substances.

Example 25: Transformation

Once a nucleic acid sequence of the invention has been cloned into an expression system, it is transformed into a plant cell. Methods for transformation and regeneration of plants are well known in the art. For example, Ti plasmid vectors have been utilized for the delivery of foreign DNA, as well as direct DNA uptake, liposomes, electroporation, micro-injection, and microprojectiles. In addition, bacteria from the genus *Agrobacterium* can be utilized to transform plant cells. Below are descriptions of representative techniques for transforming both dicotyledonous and monocotyledonous plants.

1. Transformation of Dicotyledons

Transformation techniques for dicotyledons are well known in the art and include *Agrobacterium*-based techniques and techniques that do not require *Agrobacterium*. Non-*Agrobacterium* techniques involve the uptake of exogenous genetic material directly by protoplasts or cells. This can be accomplished by PEG or electroporation mediated uptake, particle bombardment-mediated delivery, or microinjection. Examples of these techniques are described by Paszkowski *et al.*, EMBO J 3: 2717-2722 (1984), Potrykus *et al.*, Mol. Gen. Genet. 199: 169-177 (1985), Reich *et al.*, Biotechnology 4: 1001-1004 (1986), and Klein *et al.*, Nature 327: 70-73 (1987). In each case the transformed cells are regenerated to whole plants using standard techniques known in the art.

Agrobacterium-mediated transformation is a preferred technique for transformation of dicotyledons because of its high efficiency of transformation and its broad utility with many different species. *Agrobacterium* transformation typically involves the transfer of the binary vector carrying the foreign DNA of interest (*e.g.* pCIB200 or pCIB2001) to an appropriate *Agrobacterium* strain which may depend of the complement of *vir* genes carried by the host *Agrobacterium* strain either on a co-resident Ti plasmid or chromosomally (*e.g.* strain CIB542 for pCIB200 and pCIB2001 (Uknes *et al.* Plant Cell 5: 159-169 (1993)). The

transfer of the recombinant binary vector to *Agrobacterium* is accomplished by a triparental mating procedure using *E. coli* carrying the recombinant binary vector, a helper *E. coli* strain which carries a plasmid such as pRK2013 and which is able to mobilize the recombinant binary vector to the target *Agrobacterium* strain. Alternatively, the recombinant binary vector can be transferred to *Agrobacterium* by DNA transformation (Höfgen & Willmitzer, Nucl. Acids Res. 16: 9877 (1988)).

Transformation of the target plant species by recombinant *Agrobacterium* usually involves co-cultivation of the *Agrobacterium* with explants from the plant and follows protocols well known in the art. Transformed tissue is regenerated on selectable medium carrying the antibiotic or herbicide resistance marker present between the binary plasmid T-DNA borders.

Another approach to transforming plant cells with a gene involves propelling inert or biologically active particles at plant tissues and cells. This technique is disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792 all to Sanford et al. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and afford incorporation within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the desired gene. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried yeast cells, dried bacterium or a bacteriophage, each containing DNA sought to be introduced) can also be propelled into plant cell tissue.

2. Transformation of Monocotyledons

Transformation of most monocotyledon species has now also become routine. Preferred techniques include direct gene transfer into protoplasts using PEG or electroporation techniques, and particle bombardment into callus tissue. Transformations can be undertaken with a single DNA species or multiple DNA species (*i.e.* co-transformation) and both these techniques are suitable for use with this invention. Co-transformation may have the advantage of avoiding complete vector construction and of generating transgenic plants with unlinked loci for the gene of interest and the selectable marker, enabling the removal of the selectable marker in subsequent generations, should this be regarded desirable. However, a disadvantage of the use of co-transformation is the

less than 100% frequency with which separate DNA species are integrated into the genome (Schocher *et al.* Biotechnology 4: 1093-1096 (1986)).

Patent Applications EP 0 292 435, EP 0 392 225, and WO 93/07278 describe techniques for the preparation of callus and protoplasts from an elite inbred line of maize, transformation of protoplasts using PEG or electroporation, and the regeneration of maize plants from transformed protoplasts. Gordon-Kamm *et al.* (Plant Cell 2: 603-618 (1990)) and Fromm *et al.* (Biotechnology 8: 833-839 (1990)) have published techniques for transformation of A188-derived maize line using particle bombardment. Furthermore, WO 93/07278 and Koziel *et al.* (Biotechnology 11: 194-200 (1993)) describe techniques for the transformation of elite inbred lines of maize by particle bombardment. This technique utilizes immature maize embryos of 1.5-2.5 mm length excised from a maize ear 14-15 days after pollination and a PDS-1000He Biolistics device for bombardment.

Transformation of rice can also be undertaken by direct gene transfer techniques utilizing protoplasts or particle bombardment. Protoplast-mediated transformation has been described for *Japonica*-types and *Indica*-types (Zhang *et al.* Plant Cell Rep 7: 379-384 (1988); Shimamoto *et al.* Nature 338: 274-277 (1989); Datta *et al.* Biotechnology 8: 736-740 (1990)). Both types are also routinely transformable using particle bombardment (Christou *et al.* Biotechnology 9: 957-962 (1991)). Furthermore, WO 93/21335 describes techniques for the transformation of rice via electroporation.

Patent Application EP 0 332 581 describes techniques for the generation, transformation and regeneration of Pooideae protoplasts. These techniques allow the transformation of *Dactylis* and wheat. Furthermore, wheat transformation has been described by Vasil *et al.* (Biotechnology 10: 667-674 (1992)) using particle bombardment into cells of type C long-term regenerable callus, and also by Vasil *et al.* (Biotechnology 11: 1553-1558 (1993)) and Weeks *et al.* (Plant Physiol. 102: 1077-1084 (1993)) using particle bombardment of immature embryos and immature embryo-derived callus. A preferred technique for wheat transformation, however, involves the transformation of wheat by particle bombardment of immature embryos and includes either a high sucrose or a high maltose step prior to gene delivery. Prior to bombardment, any number of embryos (0.75-1 mm in length) are plated onto MS medium with 3% sucrose (Murashiga & Skoog, Physiologia Plantarum 15: 473-497 (1962)) and 3 mg/l 2,4-D for induction of somatic embryos, which is allowed to proceed in the dark. On the chosen day of bombardment, embryos are removed from the induction medium and placed onto the osmoticum (*i.e.*

induction medium with sucrose or maltose added at the desired concentration, typically 15%). The embryos are allowed to plasmolyze for 2-3 h and are then bombarded. Twenty embryos per target plate is typical, although not critical. An appropriate gene-carrying plasmid (such as pCIB3064 or pSG35) is precipitated onto micrometer size gold particles using standard procedures. Each plate of embryos is shot with the DuPont Biolistics® helium device using a burst pressure of ~1000 psi using a standard 80 mesh screen. After bombardment, the embryos are placed back into the dark to recover for about 24 h (still on osmoticum). After 24 hrs, the embryos are removed from the osmoticum and placed back onto induction medium where they stay for about a month before regeneration. Approximately one month later the embryo explants with developing embryogenic callus are transferred to regeneration medium (MS + 1 mg/liter NAA, 5 mg/liter GA), further containing the appropriate selection agent (10 mg/l basta in the case of pCIB3064 and 2 mg/l methotrexate in the case of pSOG35). After approximately one month, developed shoots are transferred to larger sterile containers known as "GA7s" which contain half-strength MS, 2% sucrose, and the same concentration of selection agent.

Tranformation of monocotyledons using *Agrobacterium* has also been described. *See,* WO 94/00977 and U.S. Patent No. 5,591,616, both of which are incorporated herein by reference.

E. Breeding and Seed Production

Example 26: Breeding

The plants obtained via tranformation with a nucleic acid sequence of the present invention can be any of a wide variety of plant species, including those of monocots and dicots; however, the plants used in the method of the invention are preferably selected from the list of agronomically important target crops set forth *supra*. The expression of a gene of the present invention in combination with other characteristics important for production and quality can be incorporated into plant lines through breeding. Breeding approaches and techniques are known in the art. See, for example, Welsh J. R., *Fundamentals of Plant Genetics and Breeding,* John Wiley & Sons, NY (1981); *Crop Breeding,* Wood D. R. (Ed.) American Society of Agronomy Madison, Wisconsin (1983); Mayo O., *The Theory of Plant Breeding,* Second Edition, Clarendon Press, Oxford (1987); Singh, D.P., *Breeding for*

Resistance to Diseases and Insect Pests, Springer-Verlag, NY (1986); and Wricke and Weber, *Quantitative Genetics and Selection Plant Breeding*, Walter de Gruyter and Co., Berlin (1986).

The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be maintained and propagated in progeny plants. Generally said maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting. Specialized processes such as hydroponics or greenhouse technologies can also be applied. As the growing crop is vulnerable to attack and damages caused by insects or infections as well as to competition by weed plants, measures are undertaken to control weeds, plant diseases, insects, nematodes, and other adverse conditions to improve yield. These include mechanical measures such a tillage of the soil or removal of weeds and infected plants, as well as the application of agrochemicals such as herbicides, fungicides, gametocides, nematicides, growth regulants, ripening agents and insecticides.

Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding, which aims at the development of plants with improved properties such as tolerance of pests, herbicides, or stress, improved nutritional value, increased yield, or improved structure causing less loss from lodging or shattering. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties, different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical, or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines, that for example, increase the effectiveness of conventional methods such as herbicide or pestidice treatment or allow one to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained, which, due to their optimized genetic "equipment", yield harvested product of

better quality than products that were not able to tolerate comparable adverse developmental conditions.

Example 27: Seed Production

In seed production, germination quality and uniformity of seeds are essential product characteristics, whereas germination quality and uniformity of seeds harvested and sold by the farmer is not important. As it is difficult to keep a crop free from other crop and weed seeds, to control seedborne diseases, and to produce seed with good germination, fairly extensive and well-defined seed production practices have been developed by seed producers, who are experienced in the art of growing, conditioning and marketing of pure seed. Thus, it is common practice for the farmer to buy certified seed meeting specific quality standards instead of using seed harvested from his own crop. Propagation material to be used as seeds is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematicides, molluscicides, or mixtures thereof. Customarily used protectant coatings comprise compounds such as captan, carboxin, thiram (TMTD®), methalaxyl (Apron®), and pirimiphos-methyl (Actellic®). If desired, these compounds are formulated together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests. The protectant coatings may be applied by impregnating propagation material with a liquid formulation or by coating with a combined wet or dry formulation. Other methods of application are also possible such as treatment directed at the buds or the fruit.

It is a further aspect of the present invention to provide new agricultural methods, such as the methods examplified above, which are characterized by the use of transgenic plants, transgenic plant material, or transgenic seed according to the present invention.

The seeds may be provided in a bag, container or vessel comprised of a suitable packaging material, the bag or container capable of being closed to contain seeds. The bag, container or vessel may be designed for either short term or long term storage, or both, of the seed. Examples of a suitable packaging material include paper, such as kraft paper, rigid or pliable plastic or other polymeric material, glass or metal. Desirably the bag, container, or vessel is comprised of a plurality of layers of packaging materials, of the same or differing type. In one embodiment the bag, container or vessel is provided so as to

exclude or limit water and moisture from contacting the seed. In one example, the bag, container or vessel is sealed, for example heat sealed, to prevent water or moisture from entering. In another embodiment water absorbent materials are placed between or adjacent to packaging material layers. In yet another embodiment the bag, container or vessel, or packaging material of which it is comprised is treated to limit, suppress or prevent disease, contamination or other adverse affects of storage or transport of the seed. An example of such treatment is sterilization, for example by chemical means or by exposure to radiation. Comprised by the present invention is a commercial bag comprising seed of a transgenic plant comprising a gene of the present invention that is expressed in said transformed plant at higher levels than in a wild type plant, together with a suitable carrier, together with label instructions for the use thereof for conferring broad spectrum disease resistance to plants.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the INTERNATIONAL DEPOSITARY AUTHORITY identified at the bottom of this page

NAME AND ADDRESS OF THE PARTY TO WHOM THE VIABILITY STATEMENT IS ISSUED

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis AG Novartis Corporation Address: 3054 Cornwallis Rd. Research Triangle Park, NC 27709	Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: *Escherichia coli* NRRL B-30077 Date of: October 28, 1998 [X] [2] Original Deposit [ ] [2] New Deposit [ ] [2] Repropagation of Original Deposit

III. (a) VIABILITY STATEMENT

Deposit was found: [X] Viable [ ] Nonviable on October 31, 1998 (Date)

International Depositary Authority's preparation was found viable on December 8, 1998 (Date)[3]

III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION

Depositor determined the International Depositary Authority's preparation was

[X] [2] Equivalent [ ] [2] Not equivalent to deposit on 1-6-99 (Date)

Signature of Depositor Hope Hart

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositors/Depositary)[4]

The dried culture was put into 2mls LB ampicillin and grown at 37°C overnight with shaking. Some of the liquid culture was streaked to an LB ampicillin plate & grown at 37°C overnight.

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): J. L. Lyon Date: 12-3-98

[1] Indicate the date of the original deposit or when a new deposit has been made.
[2] Mark with a cross the applicable box.
[3] In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.
[4] Fill in if the information has been requested.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS
OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM

Identification reference given by the DEPOSITOR:	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:
Escherichia coli pNOV2400	NRRL B-30077

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

☐ a scientific description

☒ a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on October 28, 1998(date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):
Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Date: 12 Jan 99

[1] Where Rule 6.4(d) applies, such date is the date on which the status f international depositary authority was acquired.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS
OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: *Escherichia coli* pNOV1001	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-30078

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

☐ a scientific description

☒ a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on October 28, 1998(date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: 12-3-99

[1] Where Rule 6.4(d) applies, such data is the date on which the status of international depositary authority was acquired.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION F THE DEPOSIT F MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709
NAME AND ADDRESS OF THE PARTY TO WHOM THE VIABILITY STATEMENT IS ISSUED

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the INTERNATIONAL DEPOSITARY AUTHORITY identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis AG Novartis Corporation Address: 3054 Cornwallis Rd. Research Triangle Park, NC 27709	Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: *Escherichia coli* NRRL B-30078 Date of: October 28, 1998 [X] [2] Original Deposit [ ] [2] New Deposit [ ] [2] Repropagation of Original Deposit

III. (a) VIABILITY STATEMENT

Deposit was found: [X] Viable [ ] Nonviable on October 31, 1998 (Date)

International Depositary Authority's preparation was found viable on December 8, 1998 (Date)[3]

III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION

Depositor determined the International Depositary Authority's preparation was

[X] [2] Equivalent [ ] [2] Not equivalent to deposit on 1-6-99 (Date)

Signature of Depositor Hope Hart

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositors/Depositary)[4]

The dried culture was put into 2mls LBamp(10mg/ml) and grown at 37°C overnight with shaking. Some of the liquid culture was streaked to an LBamp 10mg/ml plate and grown at 37°C overnight.

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): 12-3-98 Date:

[1] Indicate the date of the original deposit or when a new deposit has been made.
[2] Mark with a cross the applicable box.
[3] In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.
[4] Fill in if the information has been requested.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis Corp.
c/o Novartis AG
P. O. Box 12257
Research Triangle Park, NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT issued pursuant to Rule 7.1 by the INTERNATIONAL DEPOSITARY AUTHORITY identified at the bottom of this page

NAME AND ADDRESS OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: Bacteria sp. pCIB 9359-7	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-21835

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

☒ a scientific description

☐ a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on September 17, 1997 (date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: 11-13-97

[1] Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis Corp.
c/o Novartis AG
P. O. Box 12257
Research Triangle Park, NC 27709

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the INTERNATIONAL DEPOSITARY AUTHORITY identified at the bottom of this page

NAME AND ADDRESS OF THE PARTY TO WHOM THE VIABILITY STATEMENT IS ISSUED

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis Corp c/o Novartis AG Address: P. O. Box 12257 Research Triangle Park, NC 27709	Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: Bacteria sp. NRRL B-21835 Date of: September 17, 1997 ☒ [2] Original Deposit ☐ [2] New Deposit: ☐ [2] Repropagation of Original Deposit

III. (a) VIABILITY STATEMENT

Deposit was found: ☒ Viable ☐ Nonviable on September 18, 1997 (Date)

International Depositary Authority's preparation was found viable on September 25, 1997 (Date)[3]

III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION

Depositor determined the International Depositary Authority's preparation was

☐ [2] Equivalent ☐ [2] Not equivalent to deposit on _____ (Date)

Signature of Depositor _____

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositors/Depositary)[4]

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): D. 2. Lang Date: 11-(1-97

[1] Indicate the date of the original deposit or when a new deposit has been made.
[2] Mark with a cross the applicable box.
[3] In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.
[4] Fill in if the information has been requested.

What is claimed is:

1. An isolated nucleic acid molecule comprising:

(a) a nucleotide sequence substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11;

(b) a nucleotide sequence comprising nucleotides 23,768-31,336 of SEQ ID NO:11; or

(c) a nucleotide sequence isocoding with the nucleotide sequence of (a) or (b);

wherein expression of said nucleic acid molecule results in at least one toxin that is active against insects.

2. An isolated nucleic acid molecule comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11, wherein expression of said nucleic acid molecule results in at least one toxin that is active against insects.

3. An isolated nucleic acid molecule comprising a nucleotide sequence from *Photorhabdus luminescens* selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 66-1898 of SEQ ID NO:11, nucleotides 2416-9909 of SEQ ID NO:11, the complement of nucleotides 2817-3395 of SEQ ID NO:11, nucleotides 9966-14,633 of SEQ ID NO:11, nucleotides 14,699-15,007 of SEQ ID NO:11, nucleotides 15,171-18,035 of SEQ ID NO:11, the complement of nucleotides 17,072-17,398 of SEQ ID NO:11, the complement of nucleotides 18,235-19,167 of SEQ ID NO:11, the complement of nucleotides 19,385-20,116 of SEQ ID NO:11, the complement of nucleotides 20,217-20,963 of SEQ ID NO:11,

the complement of nucleotides 22,172-23,086 of SEQ ID NO:11, nucleotides 23,768-31,336 of SEQ ID NO:11, nucleotides 31,393-35,838 of SEQ ID NO:11, the complement of nucleotides 35,383-35,709 of SEQ ID NO:11, the complement of nucleotides 36,032-36,661 of SEQ ID NO:11, and the complement of nucleotides 36,654-37,781 of SEQ ID NO:11.

4. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence is substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

5. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs:2-6.

6. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence comprises nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

7. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence is substantially similar to nucleotides 15,171-18,035 or 31,393-35,838 of SEQ ID NO:11.

8. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NOs:12-14.

9. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence comprises nucleotides 15,171-18,035; 23,768-31,336; or 31,393-35,838 of SEQ ID NO:11.

10. An isolated nucleic acid molecule according to claim 2, comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides

2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

11. An isolated nucleic acid molecule according to claim 2, comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 15,171-18,035 or 31,393-35,838 of SEQ ID NO:11.

12. A chimeric gene comprising a heterologous promoter sequence operatively linked to the nucleic acid molecule of claim 1 or claim 2.

13. A recombinant vector comprising the chimeric gene of claim 12.

14. A host cell comprising the chimeric gene of claim 12.

15. A host cell according to claim 14, which is a bacterial cell.

16. A host cell according to claim 14, which is a yeast cell.

17. A host cell according to claim 14, which is a plant cell.

18. A plant comprising the plant cell of claim 17.

19. A plant according to claim 18, which is maize.

20. A toxin produced by the expression of a DNA molecule according to claim 1 or claim 2.

21. A toxin according to claim 20, wherein said toxin has activity against Lepidopteran insects.

22. A toxin according to claim 21, wherein said toxin has activity against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

23. A toxin according to claim 20, wherein said toxin has activity against Lepidopteran and Coleopteran insects.

24. A toxin according to claim 23, wherein said toxin has insecticidal activity against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

25. A toxin according to claim 20, wherein said toxin comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:2-6.

26. A toxin according to claim 20, wherein said toxin comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:12-14.

27. A composition comprising an insecticidally effective amount of a toxin according to claim 20.

28. A method of producing a toxin that is active against insects, comprising:

(a) obtaining the host cell of claim 14; and

(b) expressing the nucleic acid molecule in said cell, which results in at least one toxin that is active against insects.

29. A method of producing an insect-resistant plant, comprising introducing a nucleic acid molecule according to claim 1 into said plant, wherein said nucleic acid molecule is expressible in said plant in an effective amount to control insects.

30. A method of controlling insects comprising delivering to the insects an effective amount of a toxin according to claim 44.

31. The method of claim 29 or claim 30, wherein the insects are Lepidopteran insects.

32. The method of claim 31, wherein the insects are selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

33. The method of claim 29 or claim 30, wherein the insects are Lepidopteran and Coleopteran insects.

34. The method of claim 33, wherein the insects are selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

35. The method of claim 30, wherein the toxin is delivered to the insects orally.

36. A method for mutagenizing a nucleic acid molecule according to claim 1, wherein the nucleic acid molecule has been cleaved into population of double-stranded random fragments of a desired size, comprising:

(a) adding to the population of double-stranded random fragments one or more single- or double-stranded oligonucleotides, wherein said oligonucleotides each comprise an area of identity and an area of heterology to a double-stranded template polynucleotide;

(b) denaturing the resultant mixture of double-stranded random fragments and oligonucleotides into single-stranded fragments;

(c) incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of said single-stranded fragments at said areas of identity to form pairs of annealed fragments, said areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and

(d) repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and wherein the further cycle forms a further mutagenized double-stranded polynucleotide.

SEQUENCE LISTING

<110> Novartis AG

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<160> 22

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Met Gln
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 35                  40                  45                  50

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Lys Leu Thr His Thr Leu Ser Asp Cys Gly Lys Ala Ala Leu Lys Ala
             70                  75                  80

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Thr Tyr Gln Ala Phe Thr Gln Ala Phe Gly Val Asn Ile Ser Pro Val
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aaa tta gct cat cct atg agt aat ctt att acc atg cca agc tcc atg   849
Lys Leu Ala His Pro Met Ser Asn Leu Ile Thr Met Pro Ser Ser Met
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acg gct gca tgt tcg att atg tat gga cta cgt ggt tat caa aat acc   897
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agc ctt gat cgc tct gga ttt gta tta gcc gaa gga gcg gcg gta gtt   1137
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Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr Ile Leu
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Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile Ser Ala
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agt aaa gaa aac acg ttg ttc ggc aat acc agc gta gag aat aca atg  2006
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Lys Asn Gly Asp Lys Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu
        640                 645                 650

tat gat aaa aaa cct att ttt gta tca aag act tca att atc tct aag   2438
Tyr Asp Lys Lys Pro Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys
    655                 660                 665

atg aaa taa aaggaaagcg aaatgccaac acaaagtgat attttcactg           2487
Met Lys
670

aaataaagaa tagaatatta atgatgaagg atatagaaga tgaagaaata acaccagagt 2547

cctcttttgt ttcgcttgaa tttgatagtc ttgactatgt ggaaatccaa gtttttgtgt 2607

tggaagcgta tggtattgtg cttaaagccg aacttttttc aaatcattct atttcaacat 2667

taaatgagct cactgactat ttaaaatcaa aattgtaatc tgaattttta cttaattatg 2727

ttttttcacc attaacatta agaggttata atg aac gtt tta gaa caa ggt aag   2781
                                Met Asn Val Leu Glu Gln Gly Lys
                                    675                 680

gtt gct gct tta tat tca gcc tat tcg gaa aca gaa ggt tct tcg tgg   2829
Val Ala Ala Leu Tyr Ser Ala Tyr Ser Glu Thr Glu Gly Ser Ser Trp
                685                 690                 695

gtg gga aac ttg tgc tgt ttt tca agt gat cgg gag cat ttg cct att   2877
Val Gly Asn Leu Cys Cys Phe Ser Ser Asp Arg Glu His Leu Pro Ile
            700                 705                 710

atc gtg aat ggg cgt cgt ttc ttg att gaa ttt gtt att cca gat cat   2925
Ile Val Asn Gly Arg Arg Phe Leu Ile Glu Phe Val Ile Pro Asp His
        715                 720                 725

tta ctt gat aaa acg gtt aaa ccc aga gta ttc gat ttg gat atc aat   2973
Leu Leu Asp Lys Thr Val Lys Pro Arg Val Phe Asp Leu Asp Ile Asn
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    730                 735                 740

aaa caa ttt tta ctg cgt cgt gac cat cgt gag ata aat att tat ctt   3021
Lys Gln Phe Leu Leu Arg Arg Asp His Arg Glu Ile Asn Ile Tyr Leu
745                 750                 755                 760

tta ggt gaa gga aat ttt atg gat agg acg acg aca gat aaa aat cta   3069
Leu Gly Glu Gly Asn Phe Met Asp Arg Thr Thr Thr Asp Lys Asn Leu
                765                 770                 775

ttc gag tta aat gag gat ggt tca cta ttt att aag acg tta cgc cat   3117
Phe Glu Leu Asn Glu Asp Gly Ser Leu Phe Ile Lys Thr Leu Arg His
            780                 785                 790

gct ctt ggt aaa tat gtt gct att aat cct tca act acg caa ttt atc   3165
Ala Leu Gly Lys Tyr Val Ala Ile Asn Pro Ser Thr Thr Gln Phe Ile
        795                 800                 805

ttc ttt gca caa gga aag tac agt gaa ttt atc atg aat gcc tta aag   3213
Phe Phe Ala Gln Gly Lys Tyr Ser Glu Phe Ile Met Asn Ala Leu Lys
    810                 815                 820

aca gtt gaa gac gaa tta tca aaa cgt tat cga gtc aga att att cct   3261
Thr Val Glu Asp Glu Leu Ser Lys Arg Tyr Arg Val Arg Ile Ile Pro
825                 830                 835                 840

gaa ttg caa ggg ccg tat tat ggc ttt gaa ctt gat att ctt tct att   3309
Glu Leu Gln Gly Pro Tyr Tyr Gly Phe Glu Leu Asp Ile Leu Ser Ile
                845                 850                 855

aca gct taa ttcacaatat tatggagagt gtt atg gaa aag aaa ata aca aca 3362
Thr Ala                             Met Glu Lys Lys Ile Thr Thr
                                    860                 865

ttt acc att gag aaa act gat gac aat ttt tat gct aat ggg cgt cat   3410
Phe Thr Ile Glu Lys Thr Asp Asp Asn Phe Tyr Ala Asn Gly Arg His
            870                 875                 880

caa tgt atg gta aaa atc tct gta ctt aaa caa gaa tat agg aat ggt   3458
Gln Cys Met Val Lys Ile Ser Val Leu Lys Gln Glu Tyr Arg Asn Gly
        885                 890                 895

gat tgg ata aaa tta gca ctt agt gag gct gaa aaa aga tcg att cag   3506
Asp Trp Ile Lys Leu Ala Leu Ser Glu Ala Glu Lys Arg Ser Ile Gln
    900                 905                 910

gtg gcg gca tta agt gat agc ctc ata tat gac caa tta aaa atg cct   3554
Val Ala Ala Leu Ser Asp Ser Leu Ile Tyr Asp Gln Leu Lys Met Pro
915                 920                 925                 930

tca ggt tgg aca acg aca gat gca aga aat aaa ttt gat ctt ggg tta   3602
Ser Gly Trp Thr Thr Thr Asp Ala Arg Asn Lys Phe Asp Leu Gly Leu
                935                 940                 945

tta aat ggt gtt tat cat gct gat gct ttt att gac gaa cag gta aca   3650
Leu Asn Gly Val Tyr His Ala Asp Ala Phe Ile Asp Glu Gln Val Thr
            950                 955                 960

gat cgt gcg gga gat tgc tgc aca aat gaa aac tat cag aac agt gtg   3698
Asp Arg Ala Gly Asp Cys Cys Thr Asn Glu Asn Tyr Gln Asn Ser Val
        965                 970                 975

aaa agt gtt cct gaa att atc tat cgt tat gtc agt agt aat aga aca   3746
Lys Ser Val Pro Glu Ile Ile Tyr Arg Tyr Val Ser Ser Asn Arg Thr
    980                 985                 990
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agc aca gaa tac cta atg gca aaa atg aca ttt gaa gat acg gat ggg   3794
Ser Thr Glu Tyr Leu Met Ala Lys Met Thr Phe Glu Asp Thr Asp Gly
995                1000                1005                1010

aaa cgc aca tta aca acg aat atg tca gtt ggt gat gaa gtt ttt gac   3842
Lys Arg Thr Leu Thr Thr Asn Met Ser Val Gly Asp Glu Val Phe Asp
                1015                1020                1025

agc aag gtt tta tta aaa gcc att gct cct tat gca att aat aca aat   3890
Ser Lys Val Leu Leu Lys Ala Ile Ala Pro Tyr Ala Ile Asn Thr Asn
          1030                1035                1040

caa ttg cat gaa aac atc aat aca ttg ttt gat aaa aca gaa gag ccg   3938
Gln Leu His Glu Asn Ile Asn Thr Leu Phe Asp Lys Thr Glu Glu Pro
       1045                1050                1055

aca aaa tcc gat act cat cat caa ata att aat ctt tat cgc tgg aca   3986
Thr Lys Ser Asp Thr His His Gln Ile Ile Asn Leu Tyr Arg Trp Thr
   1060                1065                1070

ttg cca tat cat ttg agg att ctt gaa ggg aat gac agt act gtt aat   4034
Leu Pro Tyr His Leu Arg Ile Leu Glu Gly Asn Asp Ser Thr Val Asn
1075                1080                1085                1090

aga ata tat gtc ctt ggt aaa gag cca tca aat gat aga ttc ctg aca   4082
Arg Ile Tyr Val Leu Gly Lys Glu Pro Ser Asn Asp Arg Phe Leu Thr
                1095                1100                1105

aga gga agg gta ttt aaa cga gga act cat atg tga atgcacgtga        4128
Arg Gly Arg Val Phe Lys Arg Gly Thr His Met
          1110                1115

taatgtgagt ggaggatgtg ttatggacta tgcttatacc gtaactattc cggacacgca 4188

gcttgctgct gaagtgcttc atgtgacagg gtgttcgtgg acgagtggtt attatgatgg 4248

atatcatgat gtcacaatca ttgataacta cggttgtcag cataaattta gaatttcttc 4308

ggttaatatt ggacgtgcgc taagcatagc gagaataagt tgattttcct tagtaaaaaa 4368

cctttgttta tgctggtaaa cgcatgtgcg tttgccagca attaatatat tccattattg 4428

aaataggaat atagccatat ctgtaattat acataaacga atttttactc gaatataatt 4488

ttaattgatc aaacaggaaa tttaaa atg aaa gct acc gat ata tat tcc aat   4541
                          Met Lys Ala Thr Asp Ile Tyr Ser Asn
                             1120                1125

gct ttt aat ttc ggt tct tat att aat act ggt gtc gat ccc aga aca   4589
Ala Phe Asn Phe Gly Ser Tyr Ile Asn Thr Gly Val Asp Pro Arg Thr
       1130                1135                1140

ggt caa tat agt gca aat att aat att atc acg tta aga cct aat aat   4637
Gly Gln Tyr Ser Ala Asn Ile Asn Ile Ile Thr Leu Arg Pro Asn Asn
   1145                1150                1155

gtg ggt aat tcg gaa caa aca ttg agc cta tca ttc tcg cca tta aca   4685
Val Gly Asn Ser Glu Gln Thr Leu Ser Leu Ser Phe Ser Pro Leu Thr
1160                1165                1170                1175

acg tta aac aat ggc ttt ggt att ggc tgg cgc ttt tca tta aca aca   4733
Thr Leu Asn Asn Gly Phe Gly Ile Gly Trp Arg Phe Ser Leu Thr Thr
                1180                1185                1190
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tta gat ata aaa aca ctt aca ttt agc cga gca aat ggg gag caa ttt   4781
Leu Asp Ile Lys Thr Leu Thr Phe Ser Arg Ala Asn Gly Glu Gln Phe
          1195                1200                1205

aaa tgt aag cca ttg ccg cct aat aat aat gat ctt agt ttt aaa gat   4829
Lys Cys Lys Pro Leu Pro Pro Asn Asn Asn Asp Leu Ser Phe Lys Asp
      1210                1215                1220

aaa aaa cta aaa gat ttg cgc gta tat aag ctc gat agc aat act ttt   4877
Lys Lys Leu Lys Asp Leu Arg Val Tyr Lys Leu Asp Ser Asn Thr Phe
  1225                1230                1235

tat gtt tat aac aaa aac ggc att ata gag ata ctt aaa cga att ggg   4925
Tyr Val Tyr Asn Lys Asn Gly Ile Ile Glu Ile Leu Lys Arg Ile Gly
1240                1245                1250                1255

tcg agt gat att gca aaa aca gtt gca ctt gaa ttt cct gat ggt gaa   4973
Ser Ser Asp Ile Ala Lys Thr Val Ala Leu Glu Phe Pro Asp Gly Glu
             1260                1265                1270

gca ttt gat tta att tat aat tca aga ttt gca ttg tcc gaa ata aaa   5021
Ala Phe Asp Leu Ile Tyr Asn Ser Arg Phe Ala Leu Ser Glu Ile Lys
          1275                1280                1285

tac cgt gtg aca ggt aaa act tat ctt aaa ctc aat tac tct gga aat   5069
Tyr Arg Val Thr Gly Lys Thr Tyr Leu Lys Leu Asn Tyr Ser Gly Asn
      1290                1295                1300

aac tgt aca tca gtg gaa tac cct gat gat aat aat att tct gcg aaa   5117
Asn Cys Thr Ser Val Glu Tyr Pro Asp Asp Asn Asn Ile Ser Ala Lys
  1305                1310                1315

ata gca ttc gat tat cgt aac gat tac ctt att acg gtg act gta cct   5165
Ile Ala Phe Asp Tyr Arg Asn Asp Tyr Leu Ile Thr Val Thr Val Pro
1320                1325                1330                1335

tac gat gct tct ggt cct att gat tct gcc cga ttt aag atg acc tat   5213
Tyr Asp Ala Ser Gly Pro Ile Asp Ser Ala Arg Phe Lys Met Thr Tyr
             1340                1345                1350

cag aca tta aaa ggc gta ttt cca gtt atc agc acc ttc cgt aca cca   5261
Gln Thr Leu Lys Gly Val Phe Pro Val Ile Ser Thr Phe Arg Thr Pro
          1355                1360                1365

acc ggt tat gtt gag ctg gtg agt tat aaa gag aat ggg cat aaa gtg   5309
Thr Gly Tyr Val Glu Leu Val Ser Tyr Lys Glu Asn Gly His Lys Val
      1370                1375                1380

acg gac acg gaa tat att cct tat gcg gct gca ctc act att caa ccc   5357
Thr Asp Thr Glu Tyr Ile Pro Tyr Ala Ala Ala Leu Thr Ile Gln Pro
  1385                1390                1395

ggc aat gga caa cct gcg gtc agc aaa tcc tat gaa tat agt tca gta   5405
Gly Asn Gly Gln Pro Ala Val Ser Lys Ser Tyr Glu Tyr Ser Ser Val
1400                1405                1410                1415

cat aac ttc ttg ggc tat tct tct ggc cgg aca agc ttt gat tcc agt   5453
His Asn Phe Leu Gly Tyr Ser Ser Gly Arg Thr Ser Phe Asp Ser Ser
             1420                1425                1430

caa gat aat ttg tat ttg gtc aca ggg aaa tac act tat tca tcc att   5501
Gln Asp Asn Leu Tyr Leu Val Thr Gly Lys Tyr Thr Tyr Ser Ser Ile
          1435                1440                1445

gaa cgg gtt tta gat ggt caa agt gtg gtt tca gta ata gaa cga gta   5549
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Glu Arg Val Leu Asp Gly Gln Ser Val Val Ser Val Ile Glu Arg Val
      1450                1455                1460

ttt aat aaa ttc cat tta atg acc aaa gaa gca aaa aca caa gat aat   5597
Phe Asn Lys Phe His Leu Met Thr Lys Glu Ala Lys Thr Gln Asp Asn
   1465                1470                1475

aag aga att aca aca gaa att act tac aat gag gat cta tca aaa agt   5645
Lys Arg Ile Thr Thr Glu Ile Thr Tyr Asn Glu Asp Leu Ser Lys Ser
1480                1485                1490                1495

ttc tca gag caa cca gaa aat tta caa caa cct tct cgc gtg tta acc   5693
Phe Ser Glu Gln Pro Glu Asn Leu Gln Gln Pro Ser Arg Val Leu Thr
               1500                1505                1510

cgt tat acg gat ata caa aca aat act tca cga gaa gag act gtc aat   5741
Arg Tyr Thr Asp Ile Gln Thr Asn Thr Ser Arg Glu Glu Thr Val Asn
          1515                1520                1525

att aaa agt gat gat tgg gga aat act cta ctt att act gag acc agt   5789
Ile Lys Ser Asp Asp Trp Gly Asn Thr Leu Leu Ile Thr Glu Thr Ser
      1530                1535                1540

ggg ata cag aaa gaa tac gtt tat tat ccg gtc aat ggc gaa ggt aat   5837
Gly Ile Gln Lys Glu Tyr Val Tyr Tyr Pro Val Asn Gly Glu Gly Asn
   1545                1550                1555

agt tgc cct gcc gat ccc ttg ggt ttt tct cgg ttc tta aaa tca gtt   5885
Ser Cys Pro Ala Asp Pro Leu Gly Phe Ser Arg Phe Leu Lys Ser Val
1560                1565                1570                1575

acg caa aaa gga tcg cct gat gct gct caa agt gtc gca aat aaa gtg   5933
Thr Gln Lys Gly Ser Pro Asp Ala Ala Gln Ser Val Ala Asn Lys Val
               1580                1585                1590

att cat tat aca tat caa aaa ttt cct act ttt acc ggc gct tat gtt   5981
Ile His Tyr Thr Tyr Gln Lys Phe Pro Thr Phe Thr Gly Ala Tyr Val
          1595                1600                1605

aag gaa tat gtc agt aaa gtc tca gag acg ata gac aat aaa ata gcg   6029
Lys Glu Tyr Val Ser Lys Val Ser Glu Thr Ile Asp Asn Lys Ile Ala
      1610                1615                1620

aga acc ttt agc tat gtt aac tca ccg acg agt aaa tct cat ggt tcg   6077
Arg Thr Phe Ser Tyr Val Asn Ser Pro Thr Ser Lys Ser His Gly Ser
   1625                1630                1635

tta gca aaa ata acg tca gtg atg aat aac cag caa acg gtc acc aca   6125
Leu Ala Lys Ile Thr Ser Val Met Asn Asn Gln Gln Thr Val Thr Thr
1640                1645                1650                1655

ttt aaa tat gaa tat tca gaa agt gag atg acc aca aat gct acg gtg   6173
Phe Lys Tyr Glu Tyr Ser Glu Ser Glu Met Thr Thr Asn Ala Thr Val
               1660                1665                1670

acc ggt ttt gat ggc gca cat atg gaa tcg aaa aat gtg acg tct att   6221
Thr Gly Phe Asp Gly Ala His Met Glu Ser Lys Asn Val Thr Ser Ile
          1675                1680                1685

tat acc cat cgg caa ctt cgt aaa gtt gat gta aac cac gtg att acc   6269
Tyr Thr His Arg Gln Leu Arg Lys Val Asp Val Asn His Val Ile Thr
      1690                1695                1700

gat cag tct tat gat ctt ttg ggt cgc att aca ggg caa att att gat   6317
Asp Gln Ser Tyr Asp Leu Leu Gly Arg Ile Thr Gly Gln Ile Ile Asp
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1705                1710                1715

ccc ggc acg gca aga gaa att aaa cgt aat tac gtt tat caa tat ccc   6365
Pro Gly Thr Ala Arg Glu Ile Lys Arg Asn Tyr Val Tyr Gln Tyr Pro
1720              1725              1730              1735

ggc ggt gac gaa aat gat ttt tgg ccg gtg atg ata gaa gtt gat tct   6413
Gly Gly Asp Glu Asn Asp Phe Trp Pro Val Met Ile Glu Val Asp Ser
                1740              1745              1750

caa ggc gtc aga cgt aaa acc cat tac gat gga atg gga cgt att tgt   6461
Gln Gly Val Arg Arg Lys Thr His Tyr Asp Gly Met Gly Arg Ile Cys
          1755              1760              1765

tcg att gaa gaa caa gat gat gat ggc gcc tgg ggc aca tcg ggg att   6509
Ser Ile Glu Glu Gln Asp Asp Asp Gly Ala Trp Gly Thr Ser Gly Ile
      1770              1775              1780

tat caa ggc aca tat cga aaa gtt ctt gcc aga caa tat gat gtt ttg   6557
Tyr Gln Gly Thr Tyr Arg Lys Val Leu Ala Arg Gln Tyr Asp Val Leu
  1785              1790              1795

ggg cag ttg agc aag gaa att tca aat gat tgg tta tgg aat tta tct   6605
Gly Gln Leu Ser Lys Glu Ile Ser Asn Asp Trp Leu Trp Asn Leu Ser
1800              1805              1810              1815

gcc aat cct ttg gtt cgt ctt gct acc ccg ttg gtt aca acg aaa acc   6653
Ala Asn Pro Leu Val Arg Leu Ala Thr Pro Leu Val Thr Thr Lys Thr
                1820              1825              1830

tat aaa tat gat ggt tgg gga aat ctt tac agc acg gaa tac agt gat   6701
Tyr Lys Tyr Asp Gly Trp Gly Asn Leu Tyr Ser Thr Glu Tyr Ser Asp
          1835              1840              1845

ggt cgg ata gag ctg gaa atc cat gat cct att acg agg aca att act   6749
Gly Arg Ile Glu Leu Glu Ile His Asp Pro Ile Thr Arg Thr Ile Thr
      1850              1855              1860

caa ggg gtc aaa gga tta ggg atg tta aat att cag caa aat aat ttt   6797
Gln Gly Val Lys Gly Leu Gly Met Leu Asn Ile Gln Gln Asn Asn Phe
  1865              1870              1875

gag caa ccg gct tcg atc aaa gct gtg tat cct gat ggt acg ata tat   6845
Glu Gln Pro Ala Ser Ile Lys Ala Val Tyr Pro Asp Gly Thr Ile Tyr
1880              1885              1890              1895

agc acc cgt act tat cgt tat gat gga ttt ggt cgt aca gtg acg gaa   6893
Ser Thr Arg Thr Tyr Arg Tyr Asp Gly Phe Gly Arg Thr Val Thr Glu
                1900              1905              1910

aca gat gca gaa ggt cat gct acc caa att gga tat gat gtg ttt gat   6941
Thr Asp Ala Glu Gly His Ala Thr Gln Ile Gly Tyr Asp Val Phe Asp
          1915              1920              1925

cgt ata gtg aaa aaa acg ttg cca gac gga aca ata tta gaa tcc gct   6989
Arg Ile Val Lys Lys Thr Leu Pro Asp Gly Thr Ile Leu Glu Ser Ala
      1930              1935              1940

tat gca agc ttt agc cat gaa gaa tta att tcg gca ctg aac gtg aat   7037
Tyr Ala Ser Phe Ser His Glu Glu Leu Ile Ser Ala Leu Asn Val Asn
  1945              1950              1955

ggc aca cag ttg ggg gca tta gtt tat gat ggt ctt ggg cgg gta ata   7085
Gly Thr Gln Leu Gly Ala Leu Val Tyr Asp Gly Leu Gly Arg Val Ile
1960              1965              1970              1975
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agt gat acg gtg ggt ggt cgc aaa acg gaa tat tta tat ggg cct caa   7133
Ser Asp Thr Val Gly Gly Arg Lys Thr Glu Tyr Leu Tyr Gly Pro Gln
                1980                1985                1990

ggt gac aaa ccg att cag tca att act cct tcg cat aat aag caa aat   7181
Gly Asp Lys Pro Ile Gln Ser Ile Thr Pro Ser His Asn Lys Gln Asn
            1995                2000                2005

atg gat tac ctc tac tat ctt ggt agt gtg atg tcc aaa ttt acc acg   7229
Met Asp Tyr Leu Tyr Tyr Leu Gly Ser Val Met Ser Lys Phe Thr Thr
        2010                2015                2020

ggg aca gac caa caa aac ttt cgt tat cat tcg aaa acg gga aca tta   7277
Gly Thr Asp Gln Gln Asn Phe Arg Tyr His Ser Lys Thr Gly Thr Leu
    2025                2030                2035

tta tct gcg tca gaa ggc gta tct cag act aat tac agt tat ttc cca   7325
Leu Ser Ala Ser Glu Gly Val Ser Gln Thr Asn Tyr Ser Tyr Phe Pro
2040                2045                2050                2055

tcg ggt gta tta cag cga gaa tca ttt tta cgg gat aat aaa ccg att   7373
Ser Gly Val Leu Gln Arg Glu Ser Phe Leu Arg Asp Asn Lys Pro Ile
                2060                2065                2070

tca tcg ggc gag tac ctt tat acg atg tcc ggt ttg att caa cgt cat   7421
Ser Ser Gly Glu Tyr Leu Tyr Thr Met Ser Gly Leu Ile Gln Arg His
            2075                2080                2085

aaa gat agt ttt ggt cat aat cat gtt tat agt tac gat gct cag gga   7469
Lys Asp Ser Phe Gly His Asn His Val Tyr Ser Tyr Asp Ala Gln Gly
        2090                2095                2100

aga ttg gtc aaa aca gaa cag gat gca caa tac gct aca ttt gaa tat   7517
Arg Leu Val Lys Thr Glu Gln Asp Ala Gln Tyr Ala Thr Phe Glu Tyr
    2105                2110                2115

gac aat gtt ggg cga ttg ata aca acg acg acc aaa gac acg acg tca   7565
Asp Asn Val Gly Arg Leu Ile Thr Thr Thr Thr Lys Asp Thr Thr Ser
2120                2125                2130                2135

tta tcc caa tta gtg aca aaa atc gaa tat gat gct ttt gat cga gaa   7613
Leu Ser Gln Leu Val Thr Lys Ile Glu Tyr Asp Ala Phe Asp Arg Glu
                2140                2145                2150

ata aaa cgc tcg cta att agt gac ttc tca ata caa gtt att acc tta   7661
Ile Lys Arg Ser Leu Ile Ser Asp Phe Ser Ile Gln Val Ile Thr Leu
            2155                2160                2165

agc tat acg aag aat aat caa atc agt caa cgt atc acc tcc atc gat   7709
Ser Tyr Thr Lys Asn Asn Gln Ile Ser Gln Arg Ile Thr Ser Ile Asp
        2170                2175                2180

ggg gtg gtt atg aaa aat gaa cgt tat caa tat gat aat aat caa cgc   7757
Gly Val Val Met Lys Asn Glu Arg Tyr Gln Tyr Asp Asn Asn Gln Arg
    2185                2190                2195

tta agc caa tac caa tgt gag gga gaa caa tct ccg att gat cat acg   7805
Leu Ser Gln Tyr Gln Cys Glu Gly Glu Gln Ser Pro Ile Asp His Thr
2200                2205                2210                2215

ggt cgt gta tta aat cag cag att tac cat tat gac caa tgg gga aat   7853
Gly Arg Val Leu Asn Gln Gln Ile Tyr His Tyr Asp Gln Trp Gly Asn
                2220                2225                2230
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att aag cgg ctc gat aat aca tat cga gat ggt aag gaa acg gtg gat   7901
Ile Lys Arg Leu Asp Asn Thr Tyr Arg Asp Gly Lys Glu Thr Val Asp
          2235                2240                2245

tat cat ttc agt caa gcc gat cca act caa ctt att cgt att acc agc   7949
Tyr His Phe Ser Gln Ala Asp Pro Thr Gln Leu Ile Arg Ile Thr Ser
      2250                2255                2260

gac aaa cag cag ata gag tta agt tat gat gct aat ggc aac cta aca   7997
Asp Lys Gln Gln Ile Glu Leu Ser Tyr Asp Ala Asn Gly Asn Leu Thr
   2265                2270                2275

cgt gac gaa aaa ggg caa acg ctc att tac gat cag aat aat cgc ttg   8045
Arg Asp Glu Lys Gly Gln Thr Leu Ile Tyr Asp Gln Asn Asn Arg Leu
2280                2285                2290                2295

gta cag gtc aaa gac cgg ttg ggc aat ctg gtg tgc agc tac cag tat   8093
Val Gln Val Lys Asp Arg Leu Gly Asn Leu Val Cys Ser Tyr Gln Tyr
             2300                2305                2310

gat gca ttg aac aaa tta acc gca cag gtt ttg gcg aat ggt acc gtt   8141
Asp Ala Leu Asn Lys Leu Thr Ala Gln Val Leu Ala Asn Gly Thr Val
          2315                2320                2325

aat cga cag cat tat gct tcc ggt aaa gtg acg aat att caa ttg ggt   8189
Asn Arg Gln His Tyr Ala Ser Gly Lys Val Thr Asn Ile Gln Leu Gly
      2330                2335                2340

gat gaa gcg att act tgg ttg agc agt gat aag caa cga att gga cat   8237
Asp Glu Ala Ile Thr Trp Leu Ser Ser Asp Lys Gln Arg Ile Gly His
   2345                2350                2355

caa agc gcc aag aat ggt caa tca gtc tac tat caa tat ggt att gac   8285
Gln Ser Ala Lys Asn Gly Gln Ser Val Tyr Tyr Gln Tyr Gly Ile Asp
2360                2365                2370                2375

cat aac agt acg gtt atc gcc agt cag aac gaa aac gag ttg atg gct   8333
His Asn Ser Thr Val Ile Ala Ser Gln Asn Glu Asn Glu Leu Met Ala
             2380                2385                2390

tta tcc tat aca cct tat ggc ttt agg agt tta att tcc tca tta ccg   8381
Leu Ser Tyr Thr Pro Tyr Gly Phe Arg Ser Leu Ile Ser Ser Leu Pro
          2395                2400                2405

ggt ttg aat ggc gca cag gtt gat cca gta aca ggc tgg tac ttc tta   8429
Gly Leu Asn Gly Ala Gln Val Asp Pro Val Thr Gly Trp Tyr Phe Leu
      2410                2415                2420

ggt aac gga tat cgt gtt ttc aac ccg gtt ctc atg agg ttt cac agc   8477
Gly Asn Gly Tyr Arg Val Phe Asn Pro Val Leu Met Arg Phe His Ser
   2425                2430                2435

ccc gat agt tgg agt cct ttt ggt cgg gga ggg att aac cct tat acc   8525
Pro Asp Ser Trp Ser Pro Phe Gly Arg Gly Gly Ile Asn Pro Tyr Thr
2440                2445                2450                2455

tat tgc caa ggc gat ccc ata aac cgg att gat ctg aac ggt cat ctt   8573
Tyr Cys Gln Gly Asp Pro Ile Asn Arg Ile Asp Leu Asn Gly His Leu
             2460                2465                2470

agt gcc ggc ggg ata tta ggc att gtg cta ggg gca att ggc atc att   8621
Ser Ala Gly Gly Ile Leu Gly Ile Val Leu Gly Ala Ile Gly Ile Ile
          2475                2480                2485

gtc ggg att gta tca ctg gga gcc gga gcg gcg att agc gcg ggt ctc   8669
```

```
Val Gly Ile Val Ser Leu Gly Ala Gly Ala Ala Ile Ser Ala Gly Leu
      2490                2495                2500

att gct gcg ggg ggc gct ttg ggg gcg att gct tct acc agc gcg ctt   8717
Ile Ala Ala Gly Gly Ala Leu Gly Ala Ile Ala Ser Thr Ser Ala Leu
   2505                2510                2515

gca gtt act gcg act gtc att gga ttg gct gcc gat tcg ata ggg att   8765
Ala Val Thr Ala Thr Val Ile Gly Leu Ala Ala Asp Ser Ile Gly Ile
2520                2525                2530                2535

gcg tca gca gca tta tcg gaa aaa gat ccg aaa aca tct ggg ata tta   8813
Ala Ser Ala Ala Leu Ser Glu Lys Asp Pro Lys Thr Ser Gly Ile Leu
               2540                2545                2550

aat tgg att agt gcg gga ttg ggg gtt tta agc ttt ggt atc agc gca   8861
Asn Trp Ile Ser Ala Gly Leu Gly Val Leu Ser Phe Gly Ile Ser Ala
          2555                2560                2565

ata acc ttt acc tct tcg ctg gta aaa tcg gca cgg agt ggt tct cag   8909
Ile Thr Phe Thr Ser Ser Leu Val Lys Ser Ala Arg Ser Gly Ser Gln
      2570                2575                2580

gca gtc agc gcg ggt gtt atc ggg tca gtg cct ctt gaa ttt ggt gaa   8957
Ala Val Ser Ala Gly Val Ile Gly Ser Val Pro Leu Glu Phe Gly Glu
   2585                2590                2595

gtt gct agc cgt tcc agc aga cga tgg gat att gcg tta tct tcg ata   9005
Val Ala Ser Arg Ser Ser Arg Arg Trp Asp Ile Ala Leu Ser Ser Ile
2600                2605                2610                2615

tcg ttg ggc gca aat gcg gcg tct ctc tct acg ggg ata gcg gcg gcg   9053
Ser Leu Gly Ala Asn Ala Ala Ser Leu Ser Thr Gly Ile Ala Ala Ala
               2620                2625                2630

gcg gtt gca gac agt aat gcg aat gca gct aat att ctg gga tgg gta   9101
Ala Val Ala Asp Ser Asn Ala Asn Ala Ala Asn Ile Leu Gly Trp Val
          2635                2640                2645

tcc ttt ggt ttt ggt gca gta tcg aca acc tca gga ata att gag ctt   9149
Ser Phe Gly Phe Gly Ala Val Ser Thr Thr Ser Gly Ile Ile Glu Leu
      2650                2655                2660

acg cgt aca gct tat gca gtg aat cat cag act tgg gaa ctg agt tca   9197
Thr Arg Thr Ala Tyr Ala Val Asn His Gln Thr Trp Glu Leu Ser Ser
   2665                2670                2675

tca gca ggt act tcg gag gaa gtg aag cct ata cgt tgt ctc gtt tca   9245
Ser Ala Gly Thr Ser Glu Glu Val Lys Pro Ile Arg Cys Leu Val Ser
2680                2685                2690                2695

cac cgc tgg aat cag aag cag tga atgttaaccc tcctcgggca gttgagttaa  9299
His Arg Trp Asn Gln Lys Gln
               2700

tcaaacgttt cgaaatagta ccgggaacta tttagccaat cgtccattga aacccgtaat 9359

gtgttgcgac gtcgtttgac aatataaaga ttctgcgaac cgattggtta agtctcacga 9419

aaaataacta ttaggcgaca tttgcgtcgc ctttttaag gaactttatc aggttacatt 9479

tataagaagc tattttgttt tcgacggatg ttggtttctc tgagataaaa aatagaggga 9539

aatgatgtca agggtgataa tggttaattg taaaatatgt gatattattc gcatttatat 9599
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gtcaatgtaa ttcctcttat tatttaattt tattgcattt gctacgcgaa atcgccttat 9659

aattttattt ttaataaatt attatttcat cattaaacta aaataaatta tttctaga 9717

<210> 2
<211> 417
<212> PRT
<213> Photorhabdus luminescens

<400> 2

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Met Gln Arg Ala Gln Arg Val Val Ile Thr Gly Met Gly Ala Val Thr
  1               5                  10                  15

Pro Ile Gly Glu Asp Val Glu Ser Cys Trp Gln Ser Ile Ile Glu Lys
             20                  25                  30

Gln His Arg Phe His Arg Ile Glu Phe Pro Asp Ser Phe Ile Asn Ser
         35                  40                  45

Arg Phe Phe Ser Phe Leu Ala Pro Asn Pro Ser Arg Tyr Gln Leu Leu
     50                  55                  60

Pro Lys Lys Leu Thr His Thr Leu Ser Asp Cys Gly Lys Ala Ala Leu
 65                  70                  75                  80

Lys Ala Thr Tyr Gln Ala Phe Thr Gln Ala Phe Gly Val Asn Ile Ser
                 85                  90                  95

Pro Val Glu Tyr Tyr Asp Lys Tyr Glu Cys Gly Val Ile Leu Gly Ser
            100                 105                 110

Gly Trp Gly Ala Ile Asp Asn Ala Gly Asp His Ala Cys Gln Tyr Lys
        115                 120                 125

Gln Ala Lys Leu Ala His Pro Met Ser Asn Leu Ile Thr Met Pro Ser
    130                 135                 140

Ser Met Thr Ala Ala Cys Ser Ile Met Tyr Gly Leu Arg Gly Tyr Gln
145                 150                 155                 160

Asn Thr Val Met Ala Ala Cys Ala Thr Gly Thr Met Ala Ile Gly Asp
                165                 170                 175

Ala Phe Glu Ile Ile Arg Ser Gly Arg Ala Lys Cys Met Ile Ala Gly
            180                 185                 190

Ala Ala Glu Ser Leu Thr Arg Glu Cys Asn Ile Trp Ser Ile Asp Val
        195                 200                 205

Leu Asn Ala Leu Ser Lys Glu Gln Ala Asp Pro Asn Leu Ala Cys Cys
    210                 215                 220

Pro Phe Ser Leu Asp Arg Ser Gly Phe Val Leu Ala Glu Gly Ala Ala
225                 230                 235                 240

Val Val Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr
                245                 250                 255

Ile Leu Ala Glu Ile Lys Gly Tyr Ala Gln Tyr Ser Asp Ala Val Asn
            260                 265                 270

Leu Thr Arg Pro Thr Glu Asp Ile Glu Pro Lys Ile Leu Ala Ile Thr
        275                 280                 285
```

Lys Ala Ile Glu Gln Ala Gln Ile Ser Pro Lys Asp Ile Asp Tyr Ile
290 295 300

Asn Ala His Gly Thr Ser Thr Pro Leu Asn Asp Leu Tyr Glu Thr Gln
305 310 315 320

Ala Ile Lys Ala Ala Leu Gly Gln Tyr Ala Tyr Gln Val Pro Ile Ser
325 330 335

Ser Thr Lys Ser Tyr Thr Gly His Leu Ile Ala Ala Ala Gly Ser Phe
340 345 350

Glu Thr Ile Val Cys Val Lys Ala Leu Ala Glu Asn Cys Leu Pro Ala
355 360 365

Thr Leu Asn Leu His Arg Ala Asp Pro Asp Cys Asp Leu Asn Tyr Leu
370 375 380

Pro Asn Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile
385 390 395 400

Ser Ala Gly Phe Gly Gly His Asn Ala Ala Leu Val Ile Ala Lys Val
405 410 415

Arg

<210> 3
<211> 253
<212> PRT
<213> Photorhabdus luminescens

<400> 3
Met Glu Asp Ile Glu His Trp Ser Asn Phe Ser Gly Asp Phe Asn Pro
1 5 10 15

Ile His Tyr Ser Ala Lys Ser Glu Ser Leu Arg Asn Ile Gln Gln His
20 25 30

Pro Val Gln Gly Met Leu Ser Leu Leu Tyr Val Arg Gln Gln Phe Ser
35 40 45

Gln Leu Thr Ser Ala Phe Thr Thr Gly Ile Leu Asn Ile Asp Ala Ser
50 55 60

Phe Arg Gln Tyr Val Tyr Thr Ala Leu Pro His Gln Leu Arg Ile Asn
65 70 75 80

Thr Lys Asn Lys Thr Phe Lys Leu Glu Asn Pro Ser Lys Glu Asn Thr
85 90 95

Leu Phe Gly Asn Thr Ser Val Glu Asn Thr Met Glu Ser Ile Glu Asp
100 105 110

Trp Ile Val Gln Asp Asn Cys Gln Lys Leu Thr Ile Thr Gly Glu Glu
115 120 125

Val Cys Glu Lys Tyr Ala Val Phe Arg Tyr Tyr Phe Pro Ser Val Thr
130 135 140

Ser Ile Gly Trp Phe Leu Asp Ala Leu Ala Phe His Leu Ile Ile Asn
145 150 155 160

Ser Thr Gly Phe Leu Asn Phe Glu His Tyr His Phe Asn Gln Leu Gln
165 170 175

```
Asp Tyr Leu Ser Gln Ser Phe Thr Leu His Thr Gly Gln Ala Ile Lys
            180                 185                 190

Ile Arg Lys Glu Ile Val Asn Ser Thr Val Leu Leu Ser Ser Pro Asp
        195                 200                 205

Ile Cys Val Glu Leu Asn Pro Pro Leu Leu Ile Lys Asn Gly Asp Lys
    210                 215                 220

Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu Tyr Asp Lys Lys Pro
225                 230                 235                 240

Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys Met Lys
                245                 250
```

<210> 4
<211> 186
<212> PRT
<213> Photorhabdus luminescens

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<400> 4
Met Asn Val Leu Glu Gln Gly Lys Val Ala Ala Leu Tyr Ser Ala Tyr
  1               5                  10                  15

Ser Glu Thr Glu Gly Ser Ser Trp Val Gly Asn Leu Cys Cys Phe Ser
             20                  25                  30

Ser Asp Arg Glu His Leu Pro Ile Ile Val Asn Gly Arg Arg Phe Leu
         35                  40                  45

Ile Glu Phe Val Ile Pro Asp His Leu Leu Asp Lys Thr Val Lys Pro
     50                  55                  60

Arg Val Phe Asp Leu Asp Ile Asn Lys Gln Phe Leu Leu Arg Arg Asp
 65                  70                  75                  80

His Arg Glu Ile Asn Ile Tyr Leu Leu Gly Glu Gly Asn Phe Met Asp
                 85                  90                  95

Arg Thr Thr Thr Asp Lys Asn Leu Phe Glu Leu Asn Glu Asp Gly Ser
            100                 105                 110

Leu Phe Ile Lys Thr Leu Arg His Ala Leu Gly Lys Tyr Val Ala Ile
        115                 120                 125

Asn Pro Ser Thr Thr Gln Phe Ile Phe Phe Ala Gln Gly Lys Tyr Ser
    130                 135                 140

Glu Phe Ile Met Asn Ala Leu Lys Thr Val Glu Asp Glu Leu Ser Lys
145                 150                 155                 160

Arg Tyr Arg Val Arg Ile Ile Pro Glu Leu Gln Gly Pro Tyr Tyr Gly
                165                 170                 175

Phe Glu Leu Asp Ile Leu Ser Ile Thr Ala
            180                 185
```

<210> 5
<211> 258
<212> PRT
<213> Photorhabdus luminescens

<400> 5

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Met Glu Lys Lys Ile Thr Thr Phe Thr Ile Glu Lys Thr Asp
 1               5                  10

Asp Asn Phe Tyr Ala Asn Gly Arg His Gln Cys Met Val Lys Ile Ser
15                  20                  25                  30

Val Leu Lys Gln Glu Tyr Arg Asn Gly Asp Trp Ile Lys Leu Ala Leu
            35                  40                  45

Ser Glu Ala Glu Lys Arg Ser Ile Gln Val Ala Ala Leu Ser Asp Ser
        50                  55                  60

Leu Ile Tyr Asp Gln Leu Lys Met Pro Ser Gly Trp Thr Thr Thr Asp
    65                  70                  75

Ala Arg Asn Lys Phe Asp Leu Gly Leu Leu Asn Gly Val Tyr His Ala
80                  85                  90

Asp Ala Phe Ile Asp Glu Gln Val Thr Asp Arg Ala Gly Asp Cys Cys
95                  100                 105                 110

Thr Asn Glu Asn Tyr Gln Asn Ser Val Lys Ser Val Pro Glu Ile Ile
            115                 120                 125

Tyr Arg Tyr Val Ser Ser Asn Arg Thr Ser Thr Glu Tyr Leu Met Ala
        130                 135                 140

Lys Met Thr Phe Glu Asp Thr Asp Gly Lys Arg Thr Leu Thr Thr Asn
    145                 150                 155

Met Ser Val Gly Asp Glu Val Phe Asp Ser Lys Val Leu Leu Lys Ala
160                 165                 170

Ile Ala Pro Tyr Ala Ile Asn Thr Asn Gln Leu His Glu Asn Ile Asn
175                 180                 185                 190

Thr Leu Phe Asp Lys Thr Glu Glu Pro Thr Lys Ser Asp Thr His His
            195                 200                 205

Gln Ile Ile Asn Leu Tyr Arg Trp Thr Leu Pro Tyr His Leu Arg Ile
        210                 215                 220

Leu Glu Gly Asn Asp Ser Thr Val Asn Arg Ile Tyr Val Leu Gly Lys
    225                 230                 235

Glu Pro Ser Asn Asp Arg Phe Leu Thr Arg Gly Arg Val Phe Lys Arg
240                 245                 250

Gly Thr His Met
255
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<210> 6
<211> 1584
<212> PRT
<213> Photorhabdus luminescens

<400> 6

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Met Lys Ala Thr Asp Ile Tyr Ser Asn Ala Phe Asn Phe Gly Ser Tyr
 1               5                  10                  15

Ile Asn Thr Gly Val Asp Pro Arg Thr Gly Gln Tyr Ser Ala Asn Ile
            20                  25                  30
```

```
Asn Ile Ile Thr Leu Arg Pro Asn Asn Val Gly Asn Ser Glu Gln Thr
         35                  40                  45

Leu Ser Leu Ser Phe Ser Pro Leu Thr Thr Leu Asn Asn Gly Phe Gly
     50                  55                  60

Ile Gly Trp Arg Phe Ser Leu Thr Thr Leu Asp Ile Lys Thr Leu Thr
 65                  70                  75                  80

Phe Ser Arg Ala Asn Gly Glu Gln Phe Lys Cys Lys Pro Leu Pro Pro
                 85                  90                  95

Asn Asn Asn Asp Leu Ser Phe Lys Asp Lys Lys Leu Lys Asp Leu Arg
            100                 105                 110

Val Tyr Lys Leu Asp Ser Asn Thr Phe Tyr Val Tyr Asn Lys Asn Gly
        115                 120                 125

Ile Ile Glu Ile Leu Lys Arg Ile Gly Ser Ser Asp Ile Ala Lys Thr
    130                 135                 140

Val Ala Leu Glu Phe Pro Asp Gly Glu Ala Phe Asp Leu Ile Tyr Asn
145                 150                 155                 160

Ser Arg Phe Ala Leu Ser Glu Ile Lys Tyr Arg Val Thr Gly Lys Thr
                165                 170                 175

Tyr Leu Lys Leu Asn Tyr Ser Gly Asn Asn Cys Thr Ser Val Glu Tyr
            180                 185                 190

Pro Asp Asp Asn Asn Ile Ser Ala Lys Ile Ala Phe Asp Tyr Arg Asn
        195                 200                 205

Asp Tyr Leu Ile Thr Val Thr Val Pro Tyr Asp Ala Ser Gly Pro Ile
    210                 215                 220

Asp Ser Ala Arg Phe Lys Met Thr Tyr Gln Thr Leu Lys Gly Val Phe
225                 230                 235                 240

Pro Val Ile Ser Thr Phe Arg Thr Pro Thr Gly Tyr Val Glu Leu Val
                245                 250                 255

Ser Tyr Lys Glu Asn Gly His Lys Val Thr Asp Thr Glu Tyr Ile Pro
            260                 265                 270

Tyr Ala Ala Ala Leu Thr Ile Gln Pro Gly Asn Gly Gln Pro Ala Val
        275                 280                 285

Ser Lys Ser Tyr Glu Tyr Ser Ser Val His Asn Phe Leu Gly Tyr Ser
    290                 295                 300

Ser Gly Arg Thr Ser Phe Asp Ser Ser Gln Asp Asn Leu Tyr Leu Val
305                 310                 315                 320

Thr Gly Lys Tyr Thr Tyr Ser Ser Ile Glu Arg Val Leu Asp Gly Gln
                325                 330                 335

Ser Val Val Ser Val Ile Glu Arg Val Phe Asn Lys Phe His Leu Met
            340                 345                 350

Thr Lys Glu Ala Lys Thr Gln Asp Asn Lys Arg Ile Thr Thr Glu Ile
        355                 360                 365

Thr Tyr Asn Glu Asp Leu Ser Lys Ser Phe Ser Glu Gln Pro Glu Asn
    370                 375                 380
```

Leu Gln Gln Pro Ser Arg Val Leu Thr Arg Tyr Thr Asp Ile Gln Thr
385 390 395 400

Asn Thr Ser Arg Glu Glu Thr Val Asn Ile Lys Ser Asp Asp Trp Gly
405 410 415

Asn Thr Leu Leu Ile Thr Glu Thr Ser Gly Ile Gln Lys Glu Tyr Val
420 425 430

Tyr Tyr Pro Val Asn Gly Glu Gly Asn Ser Cys Pro Ala Asp Pro Leu
435 440 445

Gly Phe Ser Arg Phe Leu Lys Ser Val Thr Gln Lys Gly Ser Pro Asp
450 455 460

Ala Ala Gln Ser Val Ala Asn Lys Val Ile His Tyr Thr Tyr Gln Lys
465 470 475 480

Phe Pro Thr Phe Thr Gly Ala Tyr Val Lys Glu Tyr Val Ser Lys Val
485 490 495

Ser Glu Thr Ile Asp Asn Lys Ile Ala Arg Thr Phe Ser Tyr Val Asn
500 505 510

Ser Pro Thr Ser Lys Ser His Gly Ser Leu Ala Lys Ile Thr Ser Val
515 520 525

Met Asn Asn Gln Gln Thr Val Thr Thr Phe Lys Tyr Glu Tyr Ser Glu
530 535 540

Ser Glu Met Thr Thr Asn Ala Thr Val Thr Gly Phe Asp Gly Ala His
545 550 555 560

Met Glu Ser Lys Asn Val Thr Ser Ile Tyr Thr His Arg Gln Leu Arg
565 570 575

Lys Val Asp Val Asn His Val Ile Thr Asp Gln Ser Tyr Asp Leu Leu
580 585 590

Gly Arg Ile Thr Gly Gln Ile Ile Asp Pro Gly Thr Ala Arg Glu Ile
595 600 605

Lys Arg Asn Tyr Val Tyr Gln Tyr Pro Gly Gly Asp Glu Asn Asp Phe
610 615 620

Trp Pro Val Met Ile Glu Val Asp Ser Gln Gly Val Arg Arg Lys Thr
625 630 635 640

His Tyr Asp Gly Met Gly Arg Ile Cys Ser Ile Glu Glu Gln Asp Asp
645 650 655

Asp Gly Ala Trp Gly Thr Ser Gly Ile Tyr Gln Gly Thr Tyr Arg Lys
660 665 670

Val Leu Ala Arg Gln Tyr Asp Val Leu Gly Gln Leu Ser Lys Glu Ile
675 680 685

Ser Asn Asp Trp Leu Trp Asn Leu Ser Ala Asn Pro Leu Val Arg Leu
690 695 700

Ala Thr Pro Leu Val Thr Thr Lys Thr Tyr Lys Tyr Asp Gly Trp Gly
705 710 715 720

Asn Leu Tyr Ser Thr Glu Tyr Ser Asp Gly Arg Ile Glu Leu Glu Ile

```
                725                 730                 735

His Asp Pro Ile Thr Arg Thr Ile Thr Gln Gly Val Lys Gly Leu Gly
            740                 745                 750

Met Leu Asn Ile Gln Gln Asn Asn Phe Glu Gln Pro Ala Ser Ile Lys
        755                 760                 765

Ala Val Tyr Pro Asp Gly Thr Ile Tyr Ser Thr Arg Thr Tyr Arg Tyr
    770                 775                 780

Asp Gly Phe Gly Arg Thr Val Thr Glu Thr Asp Ala Glu Gly His Ala
785                 790                 795                 800

Thr Gln Ile Gly Tyr Asp Val Phe Asp Arg Ile Val Lys Lys Thr Leu
                805                 810                 815

Pro Asp Gly Thr Ile Leu Glu Ser Ala Tyr Ala Ser Phe Ser His Glu
            820                 825                 830

Glu Leu Ile Ser Ala Leu Asn Val Asn Gly Thr Gln Leu Gly Ala Leu
        835                 840                 845

Val Tyr Asp Gly Leu Gly Arg Val Ile Ser Asp Thr Val Gly Gly Arg
    850                 855                 860

Lys Thr Glu Tyr Leu Tyr Gly Pro Gln Gly Asp Lys Pro Ile Gln Ser
865                 870                 875                 880

Ile Thr Pro Ser His Asn Lys Gln Asn Met Asp Tyr Leu Tyr Tyr Leu
                885                 890                 895

Gly Ser Val Met Ser Lys Phe Thr Thr Gly Thr Asp Gln Gln Asn Phe
            900                 905                 910

Arg Tyr His Ser Lys Thr Gly Thr Leu Leu Ser Ala Ser Glu Gly Val
        915                 920                 925

Ser Gln Thr Asn Tyr Ser Tyr Phe Pro Ser Gly Val Leu Gln Arg Glu
    930                 935                 940

Ser Phe Leu Arg Asp Asn Lys Pro Ile Ser Ser Gly Glu Tyr Leu Tyr
945                 950                 955                 960

Thr Met Ser Gly Leu Ile Gln Arg His Lys Asp Ser Phe Gly His Asn
                965                 970                 975

His Val Tyr Ser Tyr Asp Ala Gln Gly Arg Leu Val Lys Thr Glu Gln
            980                 985                 990

Asp Ala Gln Tyr Ala Thr Phe Glu Tyr Asp Asn Val Gly Arg Leu Ile
        995                1000                1005

Thr Thr Thr Thr Lys Asp Thr Thr Ser Leu Ser Gln Leu Val Thr Lys
   1010                1015                1020

Ile Glu Tyr Asp Ala Phe Asp Arg Glu Ile Lys Arg Ser Leu Ile Ser
025                1030                1035                1040

Asp Phe Ser Ile Gln Val Ile Thr Leu Ser Tyr Thr Lys Asn Asn Gln
               1045                1050                1055

Ile Ser Gln Arg Ile Thr Ser Ile Asp Gly Val Val Met Lys Asn Glu
           1060                1065                1070
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```
Arg Tyr Gln Tyr Asp Asn Asn Gln Arg Leu Ser Gln Tyr Gln Cys Glu
      1075                1080                1085

Gly Glu Gln Ser Pro Ile Asp His Thr Gly Arg Val Leu Asn Gln Gln
   1090                1095                1100

Ile Tyr His Tyr Asp Gln Trp Gly Asn Ile Lys Arg Leu Asp Asn Thr
105                1110                1115                1120

Tyr Arg Asp Gly Lys Glu Thr Val Asp Tyr His Phe Ser Gln Ala Asp
               1125                1130                1135

Pro Thr Gln Leu Ile Arg Ile Thr Ser Asp Lys Gln Gln Ile Glu Leu
           1140                1145                1150

Ser Tyr Asp Ala Asn Gly Asn Leu Thr Arg Asp Glu Lys Gly Gln Thr
      1155                1160                1165

Leu Ile Tyr Asp Gln Asn Asn Arg Leu Val Gln Val Lys Asp Arg Leu
   1170                1175                1180

Gly Asn Leu Val Cys Ser Tyr Gln Tyr Asp Ala Leu Asn Lys Leu Thr
185                1190                1195                1200

Ala Gln Val Leu Ala Asn Gly Thr Val Asn Arg Gln His Tyr Ala Ser
               1205                1210                1215

Gly Lys Val Thr Asn Ile Gln Leu Gly Asp Glu Ala Ile Thr Trp Leu
           1220                1225                1230

Ser Ser Asp Lys Gln Arg Ile Gly His Gln Ser Ala Lys Asn Gly Gln
      1235                1240                1245

Ser Val Tyr Tyr Gln Tyr Gly Ile Asp His Asn Ser Thr Val Ile Ala
   1250                1255                1260

Ser Gln Asn Glu Asn Glu Leu Met Ala Leu Ser Tyr Thr Pro Tyr Gly
265                1270                1275                1280

Phe Arg Ser Leu Ile Ser Ser Leu Pro Gly Leu Asn Gly Ala Gln Val
               1285                1290                1295

Asp Pro Val Thr Gly Trp Tyr Phe Leu Gly Asn Gly Tyr Arg Val Phe
           1300                1305                1310

Asn Pro Val Leu Met Arg Phe His Ser Pro Asp Ser Trp Ser Pro Phe
      1315                1320                1325

Gly Arg Gly Gly Ile Asn Pro Tyr Thr Tyr Cys Gln Gly Asp Pro Ile
   1330                1335                1340

Asn Arg Ile Asp Leu Asn Gly His Leu Ser Ala Gly Gly Ile Leu Gly
345                1350                1355                1360

Ile Val Leu Gly Ala Ile Gly Ile Ile Val Gly Ile Val Ser Leu Gly
               1365                1370                1375

Ala Gly Ala Ala Ile Ser Ala Gly Leu Ile Ala Ala Gly Gly Ala Leu
           1380                1385                1390

Gly Ala Ile Ala Ser Thr Ser Ala Leu Ala Val Thr Ala Thr Val Ile
      1395                1400                1405

Gly Leu Ala Ala Asp Ser Ile Gly Ile Ala Ser Ala Ala Leu Ser Glu
   1410                1415                1420
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Lys Asp Pro Lys Thr Ser Gly Ile Leu Asn Trp Ile Ser Ala Gly Leu
425 1430 1435 1440

Gly Val Leu Ser Phe Gly Ile Ser Ala Ile Thr Phe Thr Ser Ser Leu
1445 1450 1455

Val Lys Ser Ala Arg Ser Gly Ser Gln Ala Val Ser Ala Gly Val Ile
1460 1465 1470

Gly Ser Val Pro Leu Glu Phe Gly Glu Val Ala Ser Arg Ser Ser Arg
1475 1480 1485

Arg Trp Asp Ile Ala Leu Ser Ser Ile Ser Leu Gly Ala Asn Ala Ala
1490 1495 1500

Ser Leu Ser Thr Gly Ile Ala Ala Ala Ala Val Ala Asp Ser Asn Ala
505 1510 1515 1520

Asn Ala Ala Asn Ile Leu Gly Trp Val Ser Phe Gly Phe Gly Ala Val
1525 1530 1535

Ser Thr Thr Ser Gly Ile Ile Glu Leu Thr Arg Thr Ala Tyr Ala Val
1540 1545 1550

Asn His Gln Thr Trp Glu Leu Ser Ser Ser Ala Gly Thr Ser Glu Glu
1555 1560 1565

Val Lys Pro Ile Arg Cys Leu Val Ser His Arg Trp Asn Gln Lys Gln
1570 1575 1580

<210> 7
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 7
acacagcagg ttcgtcag 18

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 8
ggcagaagca ctcaactc 18

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 9

attgatagca cgcggcgacc 20

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 10
ttgtaacgtg gagccgaact gg 22

<210> 11
<211> 37948
<212> DNA
<213> Photorhabdus luminescens

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<222> (15171)..(18035)
<223> orf5

<220>
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<222> (23768)..(31336)
<223> hph2

<220>
<221> CDS
<222> (31393)..(35838)
<223> orf2

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ccaagatgtg gtatatgcaa gcactgcatc tgttaggcga taaacctcat ctatcgttca 120

gttcagagtg gagcaaaccg agtttaggcg acgctgccgg aacggaaaga caaaagcaac 180

acgcccaagc aatggccgct ctgcgacaag gtgatgttag tcggcacaac aacccgacag 240

atcttttctt gccacaggtc aatgaagtga tgcaaaacta ttggcaaaaa ttggaacaac 300

ggctgtataa cctgcgtcat aacctcacta ttgacggcca accgctacat ctgcctattt 360

acgctacacc ggcagatcca aaagcattac ttagcgccgc tgtcgctagc tccgaaggtg 420

gggtagctct ctcacagcca tttatgtcac tgtggcgttt cccacacatg ctggaaaacg 480

cgcgtggtat ggtcagtcag ctcactcaat tcggctctac gctacaaaat attatcgaac 540

gtcaggatgc ggaagcttta aacacgctct tgcagaatca agcagcagaa ctgatattga 600

ctcatctcag catacaggac aaaaccatcg cagagctgga tgcggaaaaa atcgtactgg 660

aaaaatccaa agccggggcg caatcacgct ttgacagcta caaaaagtta tacgacgaaa 720

atatcaatgc gggtgaaaac cgggctatag cattgcatgc ctccgttgct ggcctcagca 780

ctgccctgca agcatcacgt ctggcgggcg ctgcgcttga tctggcgccc aacattttcg 840

gtctcgctga tggcggtagc cgttggggag cgattgccga agcgacaggt aatgttatgg 900

aattctccgc cagtgtgatg aacaccgaag cggataaaat cagccagtca gaagcctatc 960

gccgtcgccg tcaggaatgg gaaatccagc gtaatcatgc cgaagcagag ataaaacaga 1020

tcgatgctca acttcaatca ctggcagtac gccgtgaagc cgcggtattg cagaaagcca 1080

gcctaaaaac ccaacaggaa cagactcatg ctcaattgac tttcctgcaa cgtaaattca 1140

gtaatcaagc gttgtactac tggctacgcg gtcggctagc tgctatttac ttccaatttt 1200

acgatttggc cgtagcgcgt tgtctgatgg ctgaaatggc ttatcgttgg gagactaatg 1260

agaccgcggc aagctttatc aaaccccggcg cctggcaggg aacccatgcg ggtttactgg 1320

ctggtgaaac cttgatgctg aatctggcgc aaatggaaga tgcccatttg aggtgggatc 1380

aacgcgctct ggaagtggaa cggaccattt cattgacgca acactatgga gcactgccag 1440

aaaaatcgtt taatttagcc acacggattt ctaccctgct agcaggtggt acaactgact 1500

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Asp Asn Arg Gly Leu Thr Ile Arg Asn Ile Asp Phe His Arg Thr Thr
     20                  25                  30

gca aac ggc gat acc gat atc cgt att act cgc cat caa tat gac tcc    15320
Ala Asn Gly Asp Thr Asp Ile Arg Ile Thr Arg His Gln Tyr Asp Ser
 35                  40                  45                  50

ctt ggg cac cta agc caa agc acc gat ccg cgt cta tat gaa gcc aaa    15368
Leu Gly His Leu Ser Gln Ser Thr Asp Pro Arg Leu Tyr Glu Ala Lys
                55                  60                  65

caa aaa tct aac ttt ctc tgg cag tat gat ttg acc ggt aat att ttg    15416
Gln Lys Ser Asn Phe Leu Trp Gln Tyr Asp Leu Thr Gly Asn Ile Leu
            70                  75                  80

tgt aca gaa agc gtc gat gct ggt cgc act gtc acc ttg aat gat att    15464
Cys Thr Glu Ser Val Asp Ala Gly Arg Thr Val Thr Leu Asn Asp Ile
         85                  90                  95

gaa ggc cgt ccg cta ctg aca gta act gca aca ggt gtc ata caa acc    15512
Glu Gly Arg Pro Leu Leu Thr Val Thr Ala Thr Gly Val Ile Gln Thr
    100                 105                 110

cga caa tat gaa acg tct tcc cta ccc ggt cgt ctg ttg tct gtt acc    15560
Arg Gln Tyr Glu Thr Ser Ser Leu Pro Gly Arg Leu Leu Ser Val Thr
115                 120                 125                 130

gaa caa ata cca gaa aaa aca tcc cgt atc acc gaa cgc ctg att tgg    15608
Glu Gln Ile Pro Glu Lys Thr Ser Arg Ile Thr Glu Arg Leu Ile Trp
                135                 140                 145

gct ggc aat agc gaa gca gag aaa aac cat aat ctt gcc agc cag tgc    15656
Ala Gly Asn Ser Glu Ala Glu Lys Asn His Asn Leu Ala Ser Gln Cys
            150                 155                 160

gtg cgc cac tat gac acg gcg gga gtc acc cga tta gag agt ttg tca    15704
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Val Arg His Tyr Asp Thr Ala Gly Val Thr Arg Leu Glu Ser Leu Ser
        165                 170                 175

ctg acc ggt act gtt tta tct caa tcc agc caa cta ttg agc gac act   15752
Leu Thr Gly Thr Val Leu Ser Gln Ser Ser Gln Leu Leu Ser Asp Thr
    180                 185                 190

caa gaa gct agc tgg aca ggt gat aat gaa acc gtc tgg caa aac atg   15800
Gln Glu Ala Ser Trp Thr Gly Asp Asn Glu Thr Val Trp Gln Asn Met
195                 200                 205                 210

ctg gct gat gac atc tac aca acc ctg agc gcc ttt gat gcc acc ggc   15848
Leu Ala Asp Asp Ile Tyr Thr Thr Leu Ser Ala Phe Asp Ala Thr Gly
                215                 220                 225

gct tta ctc act cag acc gat gcg aaa ggg aac att cag agg cta acc   15896
Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly Asn Ile Gln Arg Leu Thr
            230                 235                 240

tat gat gtg gcc ggg cag cta aac ggg agc tgg tta acc tta aaa gac   15944
Tyr Asp Val Ala Gly Gln Leu Asn Gly Ser Trp Leu Thr Leu Lys Asp
        245                 250                 255

caa ccg gaa caa gtg att atc aga tcc ctg acc tat tcc gcc gcc gga   15992
Gln Pro Glu Gln Val Ile Ile Arg Ser Leu Thr Tyr Ser Ala Ala Gly
    260                 265                 270

caa aaa tta cgc gag gaa cac ggc aat ggt gtt atc acc gaa tac agt   16040
Gln Lys Leu Arg Glu Glu His Gly Asn Gly Val Ile Thr Glu Tyr Ser
275                 280                 285                 290

tat gaa ccg gaa acc caa cag ctt atc ggt acc aaa acc cac cgt ccg   16088
Tyr Glu Pro Glu Thr Gln Gln Leu Ile Gly Thr Lys Thr His Arg Pro
                295                 300                 305

tca gat gcc aaa gtg ttg caa gat cta cgt tat gag tat gac ccg gta   16136
Ser Asp Ala Lys Val Leu Gln Asp Leu Arg Tyr Glu Tyr Asp Pro Val
            310                 315                 320

ggc aat gtc atc agt atc cgt aat gac gca gaa gcc acc cgc ttc tgg   16184
Gly Asn Val Ile Ser Ile Arg Asn Asp Ala Glu Ala Thr Arg Phe Trp
        325                 330                 335

cac aat cag aaa gtg gcg ccg gaa aac act tat acc tac gac tcc ttg   16232
His Asn Gln Lys Val Ala Pro Glu Asn Thr Tyr Thr Tyr Asp Ser Leu
    340                 345                 350

tat cag ctt atc agc gca acc ggg cgc gag atg gcg aat ata ggt cag   16280
Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu Met Ala Asn Ile Gly Gln
355                 360                 365                 370

caa agt aac caa ctt ccc tcc ctc acc cta cct tct gat aac aac acc   16328
Gln Ser Asn Gln Leu Pro Ser Leu Thr Leu Pro Ser Asp Asn Asn Thr
                375                 380                 385

tac acc aac tat acc cgt act tat act tat gac cgt ggc ggc aat ttg   16376
Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr Asp Arg Gly Gly Asn Leu
            390                 395                 400

act aaa atc cag cac agt tca ccg gcg acg caa aac aac tac acc aca   16424
Thr Lys Ile Gln His Ser Ser Pro Ala Thr Gln Asn Asn Tyr Thr Thr
        405                 410                 415

aac atc acg gtt tct aac cgg agc aat cgc gca gta ctc agc act ctg   16472
Asn Ile Thr Val Ser Asn Arg Ser Asn Arg Ala Val Leu Ser Thr Leu
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    420                 425                 430

acc gaa gat ccg gcg caa gta gat gct tta ttt gat gca ggc gga cat   16520
Thr Glu Asp Pro Ala Gln Val Asp Ala Leu Phe Asp Ala Gly Gly His
435                 440                 445                 450

cag aac acg ttg ata tca gga caa aac ctg aac tgg aat aca cgc ggt   16568
Gln Asn Thr Leu Ile Ser Gly Gln Asn Leu Asn Trp Asn Thr Arg Gly
                455                 460                 465

gaa cta caa cat gtg aca ttg gtg aaa cgg gac aag ggc gcc aat gat   16616
Glu Leu Gln His Val Thr Leu Val Lys Arg Asp Lys Gly Ala Asn Asp
            470                 475                 480

gat cgg gaa tgg tat cgc tat agt agt gac ggg aga agg ata tta aaa   16664
Asp Arg Glu Trp Tyr Arg Tyr Ser Ser Asp Gly Arg Arg Ile Leu Lys
        485                 490                 495

atc aat gaa cag cag acc agc agc aac tct caa aca cag aga ata act   16712
Ile Asn Glu Gln Gln Thr Ser Ser Asn Ser Gln Thr Gln Arg Ile Thr
    500                 505                 510

tat ttg ccg agc tta gaa ctt cgt cta aca caa aac agc acg atc aca   16760
Tyr Leu Pro Ser Leu Glu Leu Arg Leu Thr Gln Asn Ser Thr Ile Thr
515                 520                 525                 530

acc gaa gat ttg caa gtt atc aca gta gga gaa gcg ggt cgg gca cag   16808
Thr Glu Asp Leu Gln Val Ile Thr Val Gly Glu Ala Gly Arg Ala Gln
                535                 540                 545

gta cga gta tta cat tgg gat agc ggt caa ccg gaa gat atc gac aat   16856
Val Arg Val Leu His Trp Asp Ser Gly Gln Pro Glu Asp Ile Asp Asn
            550                 555                 560

aat cag cta cgt tat agc tac gat aat ctt atc ggt tcc agt caa ctt   16904
Asn Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser Gln Leu
        565                 570                 575

gaa tta gac agc aaa gga gaa att att agt gag gaa gag tac tat ccc   16952
Glu Leu Asp Ser Lys Gly Glu Ile Ile Ser Glu Glu Glu Tyr Tyr Pro
    580                 585                 590

tat ggc ggc acg gca tta tgg gca aca agg aag cgg aca gaa gcc agt   17000
Tyr Gly Gly Thr Ala Leu Trp Ala Thr Arg Lys Arg Thr Glu Ala Ser
595                 600                 605                 610

tat aaa acc atc cgt tat tca ggt aaa gag cgg gat gcc acc gga cta   17048
Tyr Lys Thr Ile Arg Tyr Ser Gly Lys Glu Arg Asp Ala Thr Gly Leu
                615                 620                 625

tat tat tac ggt tac cga tat tat cag cct tgg gta gga cga tgg tta   17096
Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr Gln Pro Trp Val Gly Arg Trp Leu
            630                 635                 640

agt gcc gat ccg gca gga aca gta gat ggg ttg aat tta tat cgg atg   17144
Ser Ala Asp Pro Ala Gly Thr Val Asp Gly Leu Asn Leu Tyr Arg Met
        645                 650                 655

gta agg aat aat ccg gtt act ctg ctt gat cct gat gga tta atg cca   17192
Val Arg Asn Asn Pro Val Thr Leu Leu Asp Pro Asp Gly Leu Met Pro
    660                 665                 670

aca att gca gaa cgc ata gca gca ctg caa aaa aat aaa gta gca gat   17240
Thr Ile Ala Glu Arg Ile Ala Ala Leu Gln Lys Asn Lys Val Ala Asp
675                 680                 685                 690
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tca gcg cct tcg cca aca aat gcc aca aac gta gcg ata aac atc cgc   17288
Ser Ala Pro Ser Pro Thr Asn Ala Thr Asn Val Ala Ile Asn Ile Arg
                695                 700                 705

ccg ccc gta gca cca aaa cct acc tta ccc aaa gca tca acg agt agc   17336
Pro Pro Val Ala Pro Lys Pro Thr Leu Pro Lys Ala Ser Thr Ser Ser
            710                 715                 720

caa tca act aca tac ccc atc aaa tct gca agc ata aaa cca acg acg   17384
Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro Thr Thr
        725                 730                 735

tcg gga tca tcc att act gct cca ctg agt cca gta gga aat aaa tct   17432
Ser Gly Ser Ser Ile Thr Ala Pro Leu Ser Pro Val Gly Asn Lys Ser
    740                 745                 750

act cct gaa ata tct ctt cca gaa agc act caa agc aat tct tca agc   17480
Thr Pro Glu Ile Ser Leu Pro Glu Ser Thr Gln Ser Asn Ser Ser Ser
755                 760                 765                 770

gct att tca aca aat cta cag aaa aag tca ttt act tta tat aga gcg   17528
Ala Ile Ser Thr Asn Leu Gln Lys Lys Ser Phe Thr Leu Tyr Arg Ala
                775                 780                 785

gat aat aga tcc ttt gaa gac atg cag agt aaa ttc cct gaa gga ttt   17576
Asp Asn Arg Ser Phe Glu Asp Met Gln Ser Lys Phe Pro Glu Gly Phe
            790                 795                 800

aaa gcc tgg act cct cta gat act aag atg gca agg cag ttt gct agt   17624
Lys Ala Trp Thr Pro Leu Asp Thr Lys Met Ala Arg Gln Phe Ala Ser
        805                 810                 815

gtc ttt att ggt cag aaa gat act tct aat tta cct aaa gaa aca gtc   17672
Val Phe Ile Gly Gln Lys Asp Thr Ser Asn Leu Pro Lys Glu Thr Val
    820                 825                 830

aag aat ata aac aca tgg gga aca aaa cca aaa tta aat gat ctc tca   17720
Lys Asn Ile Asn Thr Trp Gly Thr Lys Pro Lys Leu Asn Asp Leu Ser
835                 840                 845                 850

act tac ata aaa tat acc aag gac aaa tct aca gta tgg gtc tct act   17768
Thr Tyr Ile Lys Tyr Thr Lys Asp Lys Ser Thr Val Trp Val Ser Thr
                855                 860                 865

gca att aat act gaa gca ggt gga caa agt tca ggg gct cca ctc cat   17816
Ala Ile Asn Thr Glu Ala Gly Gly Gln Ser Ser Gly Ala Pro Leu His
            870                 875                 880

gaa att aat atg gat ctt tat gag ttt acc att gac gga caa aag cta   17864
Glu Ile Asn Met Asp Leu Tyr Glu Phe Thr Ile Asp Gly Gln Lys Leu
        885                 890                 895

aat cca cta cca agg gga aga tct aaa gac agg gtg cct tca cta tta   17912
Asn Pro Leu Pro Arg Gly Arg Ser Lys Asp Arg Val Pro Ser Leu Leu
    900                 905                 910

ctt gac aca cca gaa ata gaa aca gca tcc ata att gca ctt aat cat   17960
Leu Asp Thr Pro Glu Ile Glu Thr Ala Ser Ile Ile Ala Leu Asn His
915                 920                 925                 930

gga ccg gta aat gat gca gaa gtt tca ttc cta aca aca att ccg ctt   18008
Gly Pro Val Asn Asp Ala Glu Val Ser Phe Leu Thr Thr Ile Pro Leu
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                                960                 965

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Glu Ile Pro Asp Val Leu Lys Ile Gln Cys Gly Phe Gln Cys Leu Thr
    970                 975                 980

gat att agc cac agc tct ttt aac gaa ttt cac cag caa gta tcc gaa   23902
Asp Ile Ser His Ser Ser Phe Asn Glu Phe His Gln Gln Val Ser Glu
985                 990                 995                1000

cac ctc tcc tgg tcc gaa gca cac gac tta tat cat gat gca caa cag   23950
His Leu Ser Trp Ser Glu Ala His Asp Leu Tyr His Asp Ala Gln Gln
               1005                1010                1015

gcc caa aag gat aat cgg ctg tat gaa gcg cgt att ctt aaa cgc acg   23998
Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala Arg Ile Leu Lys Arg Thr
           1020                1025                1030

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Asn Pro Gln Leu Gln Asn Ala Val His Leu Ala Ile Val Ala Pro Asn
       1035                1040                1045

gct gaa ctg ata ggc tat aac aac caa ttt agc ggc agg gcc agt caa   24094
Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln
   1050                1055                1060

tat gtc gcg ccg ggt acc gtt tcc tcc atg ttc tcc ccc gcc gct tat   24142
Tyr Val Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr
1065                1070                1075                1080

ttg act gag ctt tat cgt gaa gca cgc aat tta cac gcc agc gat tcc   24190
Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser
               1085                1090                1095

gtt tat cgc ctg gat act cgc cgc cca gat ctc aaa tca atg gcg ctc   24238
Val Tyr Arg Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu
           1100                1105                1110

agt caa caa aat atg gat acg gaa ctt tcc act ctc tct tta tcc aat   24286
Ser Gln Gln Asn Met Asp Thr Glu Leu Ser Thr Leu Ser Leu Ser Asn
       1115                1120                1125

gag cta tta ttg gaa agc att aaa act gag tct aag ctg gat aat tat   24334
Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Asp Asn Tyr
   1130                1135                1140

act caa gtg atg gaa atg ctc tcc gct ttc cgt cct tcc ggc gcg acg   24382
Thr Gln Val Met Glu Met Leu Ser Ala Phe Arg Pro Ser Gly Ala Thr
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cct tat cac gat gct tac gaa aat gtg cgt aaa gtt atc cag cta caa   24430
Pro Tyr His Asp Ala Tyr Glu Asn Val Arg Lys Val Ile Gln Leu Gln
               1165                1170                1175

gat cct ggg ctt gag caa tta aat gct tca cca gcc att gcc ggg ctg   24478
Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu
           1180                1185                1190

atg cat caa gct tcc cta tta ggt att aac gct tca atc tca cct gag   24526
Met His Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu
       1195                1200                1205

ttg ttt aat att ctg acg gag gag att act gaa ggt aat gct gag gaa   24574
Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu
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   1210                1215                1220

ctt tat aag aaa aat ttt ggt aat atc gaa ccg gct tca ctg gct atg   24622
Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met
1225              1230                1235                1240

ccg gaa tac ctt aga cgt tat tac aat tta agt gat gaa gaa ctc agc   24670
Pro Glu Tyr Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser
                1245                1250                1255

cag ttt att ggt aaa gcc agc aat ttc ggc caa caa gaa tat agt aat   24718
Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn
           1260                1265                1270

aac caa ctc att act ccg ata gtc aac agc aat gat ggc aca gtc aag   24766
Asn Gln Leu Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys
      1275                1280                1285

gta tat cga att acc cgc gaa tat aca aca aat gcc aat caa gta gac   24814
Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr Asn Ala Asn Gln Val Asp
   1290                1295                1300

gtg gag ctg ttt ccc tac ggt gga gaa aat tat cag tta aat tac aaa   24862
Val Glu Leu Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys
1305              1310                1315                1320

ttc aaa gat tct cgt cag gat gtc tcc tat tta tcc atc aaa tta aat   24910
Phe Lys Asp Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn
                1325                1330                1335

gac aaa aga gaa ctt atc cga att gaa gga gcg cct cag gtc aac atc   24958
Asp Lys Arg Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile
           1340                1345                1350

gaa tat tca gaa cat atc aca tta agt aca act gat atc agt caa cct   25006
Glu Tyr Ser Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro
      1355                1360                1365

ttt gaa atc ggc cta aca cga gta tat cct tct agt tct tgg gca tat   25054
Phe Glu Ile Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr
   1370                1375                1380

gca gcc gca aaa ttt acc att gag gaa tat aac caa tac tct ttc ctg   25102
Ala Ala Ala Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu
1385              1390                1395                1400

tta aaa ctc aat aaa gct att cgt cta tct cgt gcg aca gaa tta tca   25150
Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser
                1405                1410                1415

ccc acc att ctg gaa agt att gtg cgt agt gtt aat cag caa ctg gat   25198
Pro Thr Ile Leu Glu Ser Ile Val Arg Ser Val Asn Gln Gln Leu Asp
           1420                1425                1430

atc aac gca gaa gta tta ggt aaa gtt ttt ctg act aaa tat tat atg   25246
Ile Asn Ala Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met
      1435                1440                1445

caa cgt tat gct att aat gct gaa act gcc cta ata cta tgc aat gca   25294
Gln Arg Tyr Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala
   1450                1455                1460

ctt att tca caa cgt tca tat gat aat caa cct agc caa ttt gat cgc   25342
Leu Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg
1465              1470                1475                1480
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ctg ttt aat acg cca tta ctg aac ggc caa tat ttt tct acc gga gat   25390
Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp
               1485                1490                1495

gaa gag att gat tta aat cca ggt agt act ggc gat tgg cgt aaa tcc   25438
Glu Glu Ile Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser
          1500                1505                1510

gtg ctt aaa cgt gca ttt aat atc gat gat att tcc ctc tac cgc ctg   25486
Val Leu Lys Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu
       1515                1520                1525

ctt aaa att acc aac cat aat aat caa gat gga aag att aaa aat aac   25534
Leu Lys Ile Thr Asn His Asn Asn Gln Asp Gly Lys Ile Lys Asn Asn
   1530                1535                1540

tta aat aat ctt tct gat tta tat att ggg aaa tta ctg gca gaa att   25582
Leu Asn Asn Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile
1545                1550                1555                1560

cat caa tta acc att gat gaa ttg gat tta ttg ctg gtt gcc gtg ggt   25630
His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu Leu Val Ala Val Gly
               1565                1570                1575

gaa gga gaa act aat tta tcc gct atc agt gat aaa caa ctg gcg gca   25678
Glu Gly Glu Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala
          1580                1585                1590

ctg atc aga aaa ctc aat acc att acc gtc tgg cta cag aca cag aag   25726
Leu Ile Arg Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys
       1595                1600                1605

tgg agt gcg ttc caa tta ttt gtt atg act tcc acc agc tat aac aaa   25774
Trp Ser Ala Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys
   1610                1615                1620

acg ctg acg cct gaa att aag aat ctg ctg gat acc gtc tac cac ggt   25822
Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly
1625                1630                1635                1640

tta caa ggc ttt gat aaa gac aag gca aat tta ctg cat gtt atg gcg   25870
Leu Gln Gly Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala
               1645                1650                1655

ccc tat att gcg gcc acc tta caa tta tca tcg gaa aat gtc gcc cat   25918
Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His
          1660                1665                1670

tct gtg ctg ctt tgg gca gac aag tta aag ccc ggc gac ggc gca atg   25966
Ser Val Leu Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met
       1675                1680                1685

aca gcc gaa aaa ttc tgg gac tgg ttg aat act caa tat acg cca gat   26014
Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp
   1690                1695                1700

tca tcg gaa gta tta gca aca cag gaa cat att gtt cag tat tgt cag   26062
Ser Ser Glu Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln
1705                1710                1715                1720

gcg ttg gcg caa tta gaa atg gtt tac cat tcc acc ggt atc aat gaa   26110
Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu
               1725                1730                1735
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aac gcc ttc cgc ctg ttt gtg aca aaa cca gag atg ttt ggc tcg tca   26158
Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser
          1740                1745                1750

act gag gca gta cct gcg cat gat gca ctt tca ctg atc atg ctg acg   26206
Thr Glu Ala Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr
      1755                1760                1765

cgt ttt gca gat tgg gtt aat gcg tta ggc gaa aaa gcc tct tcc gta   26254
Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val
  1770                1775                1780

cta gcg gca ttt gaa gct aac agt tta acg gca gaa caa ttg gct gat   26302
Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp
1785                1790                1795                1800

gcc atg aat ctt gat gct aat ttg cta ttg caa gcc agt act caa gca   26350
Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala
              1805                1810                1815

caa aac cat caa cat ctt ccc cca gtg acg caa aaa aat gct ttc tcc   26398
Gln Asn His Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser
          1820                1825                1830

tgt tgg aca tct atc gac act atc ctg caa tgg gtt aat gtt gca caa   26446
Cys Trp Thr Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln
      1835                1840                1845

caa ttg aat gtc gcc cca cag gga gtt tcc gct ttg gtc ggg ctg gat   26494
Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp
  1850                1855                1860

tat att caa tta aat caa aaa atc ccc acc tat gcc cag tgg gaa agt   26542
Tyr Ile Gln Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser
1865                1870                1875                1880

gct ggg gaa ata ttg act gcc gga ttg aat tca caa cag gct gat ata   26590
Ala Gly Glu Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile
              1885                1890                1895

tta cac gct ttt ttg gac gaa tct cgc agt gcc gca tta agc acc tac   26638
Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr
          1900                1905                1910

tat atc cgt caa gtc gcc aag cca gcg gca gcc ata aaa agc cgt gat   26686
Tyr Ile Arg Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp
      1915                1920                1925

gac ttg tac caa tac tta cta att gat aat cag gtt tcc gct gca atc   26734
Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile
  1930                1935                1940

aaa act acc cgg att gcc gaa gcc att gcc agc att caa ctg tac gtc   26782
Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val
1945                1950                1955                1960

aac cgc acg ctg gaa aat gta gaa gaa aat gcc cat tca ggg gtt atc   26830
Asn Arg Thr Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile
              1965                1970                1975

agc cgt cag ttc ttt atc gac tgg gac aaa tat aac aaa cgc tac agc   26878
Ser Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser
          1980                1985                1990

acc tgg gcg ggt gtt tct caa tta gtt tac tac ccg gaa aac tat att   26926
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Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile
      1995                2000                2005

gat ccc acc atg cgt atc gga caa acc aaa atg atg gac gca tta ttg   26974
Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu
   2010                2015                2020

caa tcc gtc agc caa agc caa tta aat gcc gat act gtc gaa gac gcc   27022
Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala
2025                2030                2035                2040

ttt atg tct tat ctg aca tcg ttt gag caa gtg gct aat ctt aaa gtt   27070
Phe Met Ser Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val
               2045                2050                2055

att agc gcg tat cac gat aat att aac aac gat caa ggg ctg acc tat   27118
Ile Ser Ala Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr
          2060                2065                2070

ttt atc ggc ctc agt gaa act gat acc ggt gaa tac tat tgg cgc agt   27166
Phe Ile Gly Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser
      2075                2080                2085

gtc gat cac agt aaa ttc agc gac ggt aaa ttc gcc gct aat gcc tgg   27214
Val Asp His Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp
   2090                2095                2100

agt gaa tgg cac aaa att gat tgt cca att aat cct tac cga agc act   27262
Ser Glu Trp His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr
2105                2110                2115                2120

atc cgt cct gtg atg tac aaa tcc cgc ttg tat ctg ctc tgg ttg gaa   27310
Ile Arg Pro Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu
               2125                2130                2135

caa aag gag atc act aaa caa aca gga aat agc aaa gat ggc tat caa   27358
Gln Lys Glu Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln
          2140                2145                2150

acc gag aca gat tat cgt tat gag cta aaa ttg gcg cat atc cgt tat   27406
Thr Glu Thr Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr
      2155                2160                2165

gac ggt acc tgg aat acg cca atc act ttt gat gtc aat gaa aaa ata   27454
Asp Gly Thr Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile
   2170                2175                2180

tcc aag cta gaa ctg gca aaa aat aaa gcg cct ggg ctc tat tgt gct   27502
Ser Lys Leu Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala
2185                2190                2195                2200

ggt tat caa ggt gaa gat acg ttg ctg gtt atg ttt tat aac caa caa   27550
Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln
               2205                2210                2215

gat aca ctc gat agt tat aaa acc gct tca atg caa ggg cta tat atc   27598
Asp Thr Leu Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile
          2220                2225                2230

ttt gcc gat atg gaa tat aaa gat atg acc gat gga caa tac aaa tct   27646
Phe Ala Asp Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser
      2235                2240                2245

tat cgg gac aac agc tat aaa caa ttc gat act aat agt gtc aga aga   27694
Tyr Arg Asp Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg
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   2250                2255                2260

gtg aat aac cgc tat gca gag gat tat gaa att ccc tca tcg gta aat   27742
Val Asn Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn
2265                2270                2275                2280

agc cgt aaa ggc tat gat tgg gga gat tat tat ctc agt atg gta tat   27790
Ser Arg Lys Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr
                2285                2290                2295

aac gga gat att cca act att agt tac aaa gcc aca tca agt gat tta   27838
Asn Gly Asp Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu
           2300                2305                2310

aaa atc tat atc tcg cca aaa tta aga att att cat aat gga tat gaa   27886
Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu
       2315                2320                2325

ggg cag caa cgc aat caa tgc aat cta atg aat aaa tat ggc aaa cta   27934
Gly Gln Gln Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu
   2330                2335                2340

ggt gat aaa ttt att gtt tat act agc ttg gga gtt aat cca aat aat   27982
Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn
2345                2350                2355                2360

tcg tca aat aag ctg atg ttt tac ccc gtt tat caa tat aac gga aat   28030
Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn
                2365                2370                2375

gtc agt ggg ctt agt caa ggg aga tta cta ttc cac cgt gac acc aat   28078
Val Ser Gly Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn
           2380                2385                2390

tat tca tct aaa gta gaa gct tgg att cct gga gca gga cgt tct cta   28126
Tyr Ser Ser Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu
       2395                2400                2405

acc aat ccg aat gct gcc att ggt gat gat tat gct aca gac tcg tta   28174
Thr Asn Pro Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu
   2410                2415                2420

aac aaa ccg aat gat ctt aag caa tac gtc tat atg act gac agt aaa   28222
Asn Lys Pro Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys
2425                2430                2435                2440

ggt act gct acc gat gtc tca gga cca gta gat atc aat act gca att   28270
Gly Thr Ala Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile
                2445                2450                2455

tcc ccg gca aaa gtt cag gta aca gta aaa gcc ggt agc aaa gaa caa   28318
Ser Pro Ala Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln
           2460                2465                2470

acg ttt acc gcg gat aaa aat gtc tcc att cag cca tcc cct agc ttt   28366
Thr Phe Thr Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe
       2475                2480                2485

gat gaa atg aat tat caa ttt aat gct ctc gaa ata gat ggc tca agt   28414
Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser
   2490                2495                2500

ctg aat ttt act aac aat tca gcc agt att gat att acc ttt acc gca   28462
Leu Asn Phe Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala
2505                2510                2515                2520
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ttt gca gag gat gga cgt aaa ctg ggt tat gaa agt ttc agt att cct   28510
Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro
               2525                2530                2535

att acc cgc aag gtg agt act gat aat tcc ctg acc ctg cgc cat aat   28558
Ile Thr Arg Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn
          2540                2545                2550

gaa aat ggt gcg caa tat atg caa tgg gga gtc tat cgc att cgt ctt   28606
Glu Asn Gly Ala Gln Tyr Met Gln Trp Gly Val Tyr Arg Ile Arg Leu
       2555                2560                2565

aat act tta ttt gct cgc caa tta gtt gcg cga gcc act acc ggt att   28654
Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile
   2570                2575                2580

gat acg att ctg agt atg gaa act cag aat att cag gaa cca cag tta   28702
Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu
2585                2590                2595                2600

ggc aaa ggt ttc tac gct acg ttc gtg ata cct ccg tat aac cca tca   28750
Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser
               2605                2610                2615

act cat ggt gat gaa cgt tgg ttt aag ctt tat atc aaa cat gtt gtt   28798
Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val
          2620                2625                2630

gat aat aat tca cat att atc tat tca ggt cag cta aaa gat aca aat   28846
Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln Leu Lys Asp Thr Asn
       2635                2640                2645

ata agc acc acg tta ttt atc cct ctt gat gat gtt cca ttg aac caa   28894
Ile Ser Thr Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln
   2650                2655                2660

gat tac agc gcc aag gtt tac atg acc ttc aag aaa tca cca tca gat   28942
Asp Tyr Ser Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp
2665                2670                2675                2680

ggt acc tgg tgg ggc cct cac ttt gtt aga gat gat aaa gga ata gta   28990
Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val
               2685                2690                2695

aca ata aac cct aaa tcc att ttg acc cac ttt gag agc gtc aat gtc   29038
Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val
          2700                2705                2710

ctg aat aat att agt agc gaa cca atg gat ttc agc ggc gct aac agc   29086
Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser
       2715                2720                2725

ctc tat ttt tgg gaa ctg ttc tac tat acc ccg atg ctg gtt gcc caa   29134
Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln
   2730                2735                2740

cgt ttg ttg cat gag caa aac ttt gat gaa gcg aac cgc tgg ctg aaa   29182
Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys
2745                2750                2755                2760

tat gtc tgg agc cca tcc ggg tat att gtt cac ggc cag att cag aat   29230
Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn
               2765                2770                2775
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tat caa tgg aac gtc cgc ccg tta ttg gaa gat acc agt tgg aac agt   29278
Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser
          2780                2785                2790

gat cct ttg gat tcc gtc gat cct gac gcg gta gcg cag cac gat ccg   29326
Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro
       2795                2800                2805

atg cac tat aaa gtt tca acc ttt atg cgc acc ctt gat ctg ttg atc   29374
Met His Tyr Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile
   2810                2815                2820

gcg cgc ggc gac cat gct tac cgc caa ttg gag cgc gat acg ctt aac   29422
Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn
2825                2830                2835                2840

gaa gcg aag atg tgg tat atg caa gcg ctg cat ctg tta ggc gat aaa   29470
Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys
               2845                2850                2855

cct tat ctg ccg ctg agt acc aca tgg aat gat cca cga ctg gac aaa   29518
Pro Tyr Leu Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys
          2860                2865                2870

gcc gcg gat att act acc caa agt gct cat tcc agc tca ata gtc gct   29566
Ala Ala Asp Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala
       2875                2880                2885

ttg cgg cag agt aca ccg gcg ctt tta tca ttg cgc agc gcc aat acc   29614
Leu Arg Gln Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr
   2890                2895                2900

ctg acc gat ctc ttc ctg ccg caa atc aat gaa gtg atg atg aat tac   29662
Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr
2905                2910                2915                2920

tgg caa aca tta gct cag aga gta tac aac ctg cgc cac aac ctc tct   29710
Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser
               2925                2930                2935

atc gac ggt cag ccg tta tat ctg cca atc tat gcc aca ccg gcg gac   29758
Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp
          2940                2945                2950

ccg aaa gcg tta ctc agc gcc gct gtt gcc act tct caa ggt gga ggc   29806
Pro Lys Ala Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly
       2955                2960                2965

aag ctg ccg gag tca ttt atg tcc ctg tgg cgt ttc ccg cac atg ctg   29854
Lys Leu Pro Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu
   2970                2975                2980

gaa aat gct cgc agc atg gtt agc cag ctc acc caa ttc ggc tcc acg   29902
Glu Asn Ala Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr
2985                2990                2995                3000

tta caa aat att atc gaa cgt cag gac gca gaa gcg ctc aat gcg tta   29950
Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala Glu Ala Leu Asn Ala Leu
               3005                3010                3015

tta caa aat cag gcc gca gag ctg ata ttg act aac ctg agt att caa   29998
Leu Gln Asn Gln Ala Ala Glu Leu Ile Leu Thr Asn Leu Ser Ile Gln
          3020                3025                3030

gac aaa acc att gaa gaa ctg gat gcc gag aaa acc gtg ctg gaa aaa   30046
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Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys
      3035                3040                3045

tcc aaa gcg gga gca caa tcg cgc ttt gat agc tat agc aaa ctg cat   30094
Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His
   3050                3055                3060

gat gaa aac atc aac gcc ggt gaa aac caa gct atg acg cta cga gcg   30142
Asp Glu Asn Ile Asn Ala Gly Glu Asn Gln Ala Met Thr Leu Arg Ala
3065                3070                3075                3080

tcc gca gcc ggg ctt acc acg gcg gtt cag gca tcc cgt ctg gcc ggc   30190
Ser Ala Ala Gly Leu Thr Thr Ala Val Gln Ala Ser Arg Leu Ala Gly
                3085                3090                3095

gca gcg gct gat ctg gtg cct aac atc ttc ggc ttc gcc ggt ggt ggt   30238
Ala Ala Ala Asp Leu Val Pro Asn Ile Phe Gly Phe Ala Gly Gly Gly
           3100                3105                3110

agc cgt tgg ggg gct atc gct gag gcg acc ggc tat gta atg gaa ttt   30286
Ser Arg Trp Gly Ala Ile Ala Glu Ala Thr Gly Tyr Val Met Glu Phe
      3115                3120                3125

tcc gct aat gtt atg aat acc gaa gcg gat aaa att agc caa tct gaa   30334
Ser Ala Asn Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu
   3130                3135                3140

acc tac cgt cgt cgc cgt cag gag tgg gaa att cag cgt aat aat gcc   30382
Thr Tyr Arg Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala
3145                3150                3155                3160

gaa gcg gag ctg aaa caa ctc gat gcc caa ctt aaa tcg ctg gca gta   30430
Glu Ala Glu Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val
                3165                3170                3175

cgc cgt gaa gcc gcc gta ttg caa aaa acc agc ctg aaa acc caa caa   30478
Arg Arg Glu Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln
           3180                3185                3190

gag cag acc caa gcc caa ttg gcc ttc ctg caa cgt aag ttc agc aat   30526
Glu Gln Thr Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn
      3195                3200                3205

caa gcg ttg tac aac tgg cta cgt ggc cga ctg gca gca att tac ttc   30574
Gln Ala Leu Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Phe
   3210                3215                3220

caa ttc tac gac ttg gct atc gcg cgt tgt tta atg gca gag cag gct   30622
Gln Phe Tyr Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala
3225                3230                3235                3240

tac cgt tgg gaa att agc gat gac tct gct cgc ttt att aaa ccg ggc   30670
Tyr Arg Trp Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly
                3245                3250                3255

gcc tgg caa gga acc tat gca ggt ctg ctg gca ggt gaa acc ttg atg   30718
Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met
           3260                3265                3270

cta agt ttg gca caa atg gaa gac gcc cat tta aga cgc gat aaa cgc   30766
Leu Ser Leu Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg
      3275                3280                3285

gca tta gag gtc gaa cgt aca gta tcg ctg gcc gaa att tat gct ggt   30814
Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly
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3290                3295                3300

tta ccg caa gat aaa ggc cca ttc tcc ctg acg caa gaa atc gag aag   30862
Leu Pro Gln Asp Lys Gly Pro Phe Ser Leu Thr Gln Glu Ile Glu Lys
3305                3310                3315                3320

ctg gtg aat gca ggt tca ggc agc gcc ggc agt ggt aat aat aat ttg   30910
Leu Val Asn Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu
                3325                3330                3335

gca ttt ggc gcc ggc acg gac act aaa act tct ttg cag gca tcc att   30958
Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile
            3340                3345                3350

tca tta gct gat tta aaa att cgt gag gat tac ccg gaa tct att ggc   31006
Ser Leu Ala Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly
        3355                3360                3365

aaa atc cga cgc atc aaa cag atc agc gtt acc ctg ccg gcg cta ttg   31054
Lys Ile Arg Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Leu
    3370                3375                3380

gga cct tat cag gat gtg cag gca ata tta tct tac ggc gat aaa gcc   31102
Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Asp Lys Ala
3385                3390                3395                3400

gga tta gcg aac ggc tgt gca gcg ctg gcc gtt tcc cac ggt acg aat   31150
Gly Leu Ala Asn Gly Cys Ala Ala Leu Ala Val Ser His Gly Thr Asn
                3405                3410                3415

gac agc ggt caa ttc cag ctc gat ttc aac gat ggc aaa ttc ctg ccg   31198
Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Phe Leu Pro
            3420                3425                3430

ttt gaa ggt atc gcc att gat caa ggt acg cta aca ctg agt ttt cct   31246
Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro
        3435                3440                3445

aat gca tca acg cca gcc aaa ggt aaa caa gcc act atg tta aaa acc   31294
Asn Ala Ser Thr Pro Ala Lys Gly Lys Gln Ala Thr Met Leu Lys Thr
    3450                3455                3460

ctg aac gat atc att ttg cat att cgc tac acc att aag taa           31336
Leu Asn Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Lys
3465                3470                3475

ccatcccaac acagaactaa gacaggcccc gaatcggggt ctggtaagga gtttct atg 31395
                                                              Met

cag aat tca cag aca ttc agc atg acc gag ctg tca tta cct aag ggc   31443
Gln Asn Ser Gln Thr Phe Ser Met Thr Glu Leu Ser Leu Pro Lys Gly
3480                3485                3490                3495

ggc ggc gcc att acc ggt atg ggt gaa gca tta acg ccg gcc ggg ccg   31491
Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Ala Gly Pro
                3500                3505                3510

gat ggt atg gca gcc tta tcg ctg cca ttg ccc att tct gcc gga cgt   31539
Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly Arg
            3515                3520                3525

ggt tat gcc ccc tcg ctc acg ctg aac tac aac agc gga acc ggt aac   31587
Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly Asn
        3530                3535                3540
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agc ccg ttc ggt ctc ggt tgg gac tgt aac gtc atg aca att cgt cgt   31635
Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg Arg
   3545                3550                3555

cgc acc agt acc ggc gtg ccg aat tat gat gaa acc gat act ttt ctg   31683
Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe Leu
3560               3565                3570                3575

ggg ccg gaa ggt gaa gtg ttg gtc gta gca tta aat gag gca ggt caa   31731
Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly Gln
               3580                3585                3590

gct gat atc cgc agt gaa tcc tca tta cag ggc atc aat ttg ggg atg   31779
Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly Met
          3595                3600                3605

acc ttc acc gtt acc ggt tat cgc tcc cgt ttg gaa agc cac ttt agc   31827
Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe Ser
       3610                3615                3620

cgg ttg gaa tac tgg caa ccc caa aca aca ggc gca acc gat ttc tgg   31875
Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe Trp
   3625                3630                3635

ctg ata tac agc ccc gac gga caa gcc cat tta ctg ggc aaa aat cct   31923
Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn Pro
3640               3645                3650                3655

caa gca cgc atc agc aat cca cta aat gtt aac caa aca gcg caa tgg   31971
Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln Trp
               3660                3665                3670

cta ttg gaa gcc tcg gta tca tcc cac ggc gag cag att tat tat cag   32019
Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr Gln
          3675                3680                3685

tat cga gcc gaa gat gaa act gat tgc gaa act gac gaa ctc aca gcc   32067
Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr Ala
       3690                3695                3700

cac ccg aac aca acc gtc cag cgc tac ctg caa gta gta cat tac ggt   32115
His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr Gly
   3705                3710                3715

aat cta acc gcc agc gaa gta ttt ccc acg cta aat gga gat gat cca   32163
Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp Pro
3720               3725                3730                3735

ctc aaa tct ggc tgg ttg ttc tgt tta gta ttt gat tac ggt gag cgc   32211
Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu Arg
               3740                3745                3750

aaa aac agc tta tct gaa atg ccg cca ttt aaa gcc aca agt aac tgg   32259
Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn Trp
          3755                3760                3765

ctt tgc cgc aaa gac cgt ttt tcc cgt tat gaa tac ggt ttt gca ttg   32307
Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala Leu
       3770                3775                3780

cgc acc cgg cgc tta tgt cgc caa ata ctg atg ttt cac cgt ctg caa   32355
Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu Gln
   3785                3790                3795

acc ctg tct ggt cag gca aaa ggc gac gat gaa ccc gca tta gtt tca   32403
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Thr Leu Ser Gly Gln Ala Lys Gly Asp Asp Glu Pro Ala Leu Val Ser
3800                3805                3810                3815

cgt ctg ata ctg gat tat gac gaa aac gcg gtg gtc agt acg ctc gtt   32451
Arg Leu Ile Leu Asp Tyr Asp Glu Asn Ala Val Val Ser Thr Leu Val
                3820                3825                3830

tct gtc cgc cga gtg gga cat gag caa gat ggc aca acg gcg gtc gcc   32499
Ser Val Arg Arg Val Gly His Glu Gln Asp Gly Thr Thr Ala Val Ala
           3835                3840                3845

ctg ccg cca ttg gaa ctg gct tat cag cct ttt gaa cca gaa caa aaa   32547
Leu Pro Pro Leu Glu Leu Ala Tyr Gln Pro Phe Glu Pro Glu Gln Lys
       3850                3855                3860

gca ctc tgg cga cca atg gat gta ctg gcg aat ttc aac acc atc caa   32595
Ala Leu Trp Arg Pro Met Asp Val Leu Ala Asn Phe Asn Thr Ile Gln
   3865                3870                3875

cgc tgg caa ctg ctt gat ctg caa ggc gaa ggc gta ccc ggt att ctg   32643
Arg Trp Gln Leu Leu Asp Leu Gln Gly Glu Gly Val Pro Gly Ile Leu
3880                3885                3890                3895

tat cag gat aaa aat ggc tgg tgg tat cga tct gct caa cgt cag aca   32691
Tyr Gln Asp Lys Asn Gly Trp Trp Tyr Arg Ser Ala Gln Arg Gln Thr
                3900                3905                3910

ggg gaa gag atg aat gcg gtc acc tgg ggc aaa atg caa ctc ctt cct   32739
Gly Glu Glu Met Asn Ala Val Thr Trp Gly Lys Met Gln Leu Leu Pro
           3915                3920                3925

atc acg ccc gct att cag gat aac gcc tca ctg atg gat att aat ggt   32787
Ile Thr Pro Ala Ile Gln Asp Asn Ala Ser Leu Met Asp Ile Asn Gly
       3930                3935                3940

gat ggg caa ctg gat tgg gtt atc acc ggt ccg ggg cta agg ggt tat   32835
Asp Gly Gln Leu Asp Trp Val Ile Thr Gly Pro Gly Leu Arg Gly Tyr
   3945                3950                3955

cac agc cag cat cca gat ggc agt tgg aca cgt ttt acg ccg ttg cac   32883
His Ser Gln His Pro Asp Gly Ser Trp Thr Arg Phe Thr Pro Leu His
3960                3965                3970                3975

gcc tta ccg ata gaa tat acc cat ccc cgc gcc caa ctt gcg gat tta   32931
Ala Leu Pro Ile Glu Tyr Thr His Pro Arg Ala Gln Leu Ala Asp Leu
                3980                3985                3990

atg ggg gcc ggg ctg tcc gat tta gtg ctg att ggt ccc aaa agc gtg   32979
Met Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro Lys Ser Val
           3995                4000                4005

cgt ttg tat gcc aat aac cgt gat ggt ttt acc gaa gga cgg gat gtg   33027
Arg Leu Tyr Ala Asn Asn Arg Asp Gly Phe Thr Glu Gly Arg Asp Val
       4010                4015                4020

gtg caa tcc ggt ggt atc acc ctg ccg tta ccg ggc gcc gat gcg cgt   33075
Val Gln Ser Gly Gly Ile Thr Leu Pro Leu Pro Gly Ala Asp Ala Arg
   4025                4030                4035

aag tta gtg gcc ttt agc gac gta ctc ggt tca ggc caa gca cat ttg   33123
Lys Leu Val Ala Phe Ser Asp Val Leu Gly Ser Gly Gln Ala His Leu
4040                4045                4050                4055

gtt gaa gtt agt gcg acg aaa gtc acc tgc tgg cca aat ctg gga cat   33171
Val Glu Val Ser Ala Thr Lys Val Thr Cys Trp Pro Asn Leu Gly His
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                4060                4065                4070

ggc cgt ttt ggt cag cca atc aca ttg ccg gga ttt agc caa tcc gcc   33219
Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser Ala
            4075                4080                4085

gcc aat ttt aat cct gat cga gtt cat ctg gcc gat ctg gac ggt agt   33267
Ala Asn Phe Asn Pro Asp Arg Val His Leu Ala Asp Leu Asp Gly Ser
        4090                4095                4100

ggt cct gcc gat ctg att tat gtt cat gct gac cat ctg gat att ttc   33315
Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile Phe
    4105                4110                4115

agc aat gaa agt ggt aac ggt ttt gca caa cca ttc aca ctc cgt ttt   33363
Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg Phe
4120                4125                4130                4135

cct gac ggc ctg cgt ttt gat gat act tgc cag cta caa gtg gct gat   33411
Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala Asp
                4140                4145                4150

gta cag gga tta ggg gtt gtc agc ctg atc ctg agc gta ccg cat atg   33459
Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His Met
            4155                4160                4165

gcg cca cac cat tgg cgc tgc gat ctg acc aac gcg aaa ccg tgg tta   33507
Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp Leu
        4170                4175                4180

ctc agt gaa atg aac aac aac atg gga gcc cat cac acc ctg cat tac   33555
Leu Ser Glu Met Asn Asn Asn Met Gly Ala His His Thr Leu His Tyr
    4185                4190                4195

cgt agc tcc gtc cag ttt tgg ctg gat gaa aaa gcc gca gcc tta gct   33603
Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu Ala
4200                4205                4210                4215

acc gga caa aca ccg gtc tgt tac ctg ccc ttc ccg gtc cat acc ctg   33651
Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr Leu
                4220                4225                4230

tgg caa aca gaa acc gag gat gaa atc agc ggc aat aaa tta gtg acc   33699
Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val Thr
            4235                4240                4245

act tta cgt tac gct cac ggc gcc tgg gat gga cgt gag cgg gaa ttt   33747
Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu Phe
        4250                4255                4260

cgc ggc ttt ggc tat gtt gag cag aca gac agc cat caa ctg gct caa   33795
Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Gln Leu Ala Gln
    4265                4270                4275

ggc aat gcg ccg gaa cgt aca tca ccg gca ctt acc aaa aac tgg tat   33843
Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp Tyr
4280                4285                4290                4295

gcc acc gga atc cct gag gta gac aat acg cta tct gcc ggg tat tgg   33891
Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr Trp
                4300                4305                4310

cgc ggt gat acg cag gct ttc act ggt ttt acg cca cac ttt act ctc   33939
Arg Gly Asp Thr Gln Ala Phe Thr Gly Phe Thr Pro His Phe Thr Leu
            4315                4320                4325
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tgg aaa gag ggc aaa gat gtt cca ctg aca ccg gaa gat gac cac aat   33987
Trp Lys Glu Gly Lys Asp Val Pro Leu Thr Pro Glu Asp Asp His Asn
      4330                4335                4340

ctg tac tgg tta aac cgg gca cta aaa ggt caa cca ctg cgt agt gaa   34035
Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser Glu
   4345                4350                4355

ctc tac ggg cta gat ggc agc gca cag cag aag atc ccc tat aca gtg   34083
Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr Val
4360                4365                4370                4375

act gaa tcc cgc cca caa gtg cgc caa tta caa gat aac act acc ctt   34131
Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr Leu
               4380                4385                4390

tcc ccg gtg ctc tgg gcc tca gtg gtg gaa agt cgt agt tat cac tat   34179
Ser Pro Val Leu Trp Ala Ser Val Val Glu Ser Arg Ser Tyr His Tyr
          4395                4400                4405

gaa cgt atc atc agc gat ccc caa tgc aat cag gat atc act ctg tcc   34227
Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu Ser
      4410                4415                4420

agt gac cta ttc ggg caa ccg ctg aaa cag gtt tca gtg caa tat ccc   34275
Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr Pro
   4425                4430                4435

cgc cgc aat aaa cca aca acc aat ccg tat ccc gat aca cta cca gat   34323
Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro Asp
4440                4445                4450                4455

act ctg ttt gcc agc agt tat gac gac caa caa caa cta ttg cgg tta   34371
Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg Leu
               4460                4465                4470

acc tac cag caa tcc agt tgg cat cat cta att gct aat gaa ctc aga   34419
Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu Arg
          4475                4480                4485

gtg tta gga tta ccg gat ggt aca cgc agt gat gct ttc act tac gat   34467
Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr Asp
      4490                4495                4500

gct aaa cac gtg cct gtt gat ggt tta aat ctg gaa gct cta tgt gct   34515
Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys Ala
   4505                4510                4515

gaa aat agc ctg att gcc gat gat aaa cct cgc gaa tac ctc aac cag   34563
Glu Asn Ser Leu Ile Ala Asp Asp Lys Pro Arg Glu Tyr Leu Asn Gln
4520                4525                4530                4535

caa cga acg ttc tat acc gat ggg aaa acc gat gga aaa aat cca acg   34611
Gln Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro Thr
               4540                4545                4550

cca ctg aaa aca ccg aca cga cag gct tta atc gcc ttt acc gaa acg   34659
Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu Thr
          4555                4560                4565

gcg gta tta acg gaa tct ctg tta tcc gca ttt gat ggc ggt atc acg   34707
Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Phe Asp Gly Gly Ile Thr
      4570                4575                4580
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cca gat gaa tta ccc ggc ctt ctg aca caa gca gga tac caa caa gaa   34755
Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln Glu
   4585                4590                4595

cct tat ctg ttc cca ctc agt ggc gaa aac caa gtc tgg gta gca cgc   34803
Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala Arg
4600                4605                4610                4615

aaa ggc tat acc gat tac gga act gag gta caa ttt tgg cgt cct gtc   34851
Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro Val
                4620                4625                4630

gca caa cgt aac acc cag tta acc ggg aaa acg act cta aaa tgg gat   34899
Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp Asp
           4635                4640                4645

acc cac tac tgt gtc atc act caa acc caa gac gcg gct ggt ttg act   34947
Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu Thr
       4650                4655                4660

gtc tca gcc aat tat gac tgg cgt ttt ctc aca cct atg caa ctg act   34995
Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu Thr
   4665                4670                4675

gat atc aac gat aat gtg cat atc ata acc ttg gat gcg cta gga cgc   35043
Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly Arg
4680                4685                4690                4695

cct gtc act caa cgt ttc tgg gga atc gaa aat ggt gtg gca aca ggt   35091
Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr Gly
                4700                4705                4710

tac tct tca cca gaa gca aaa cca ttc act cca cca gtc gat gtc aat   35139
Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val Asn
           4715                4720                4725

gct gcc att gct ctg acc gga cca ctc cct gtc gcg cag tgt ctg gtc   35187
Ala Ala Ile Ala Leu Thr Gly Pro Leu Pro Val Ala Gln Cys Leu Val
       4730                4735                4740

tat gcg ccg gac agt tgg atg ccg cta ttc ggt cag gaa acc ttc aac   35235
Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe Asn
   4745                4750                4755

aca tta acg cag gaa gag caa aag aca ctg cgt gat tta cgg att atc   35283
Thr Leu Thr Gln Glu Glu Gln Lys Thr Leu Arg Asp Leu Arg Ile Ile
4760                4765                4770                4775

aca gaa gat tgg cgt att tgc gca ctg gct cgc cgc cgt tgg cta caa   35331
Thr Glu Asp Trp Arg Ile Cys Ala Leu Ala Arg Arg Arg Trp Leu Gln
                4780                4785                4790

agt caa aaa gcc ggc aca cca ttg gtt aag ctg tta acc aac agc atc   35379
Ser Gln Lys Ala Gly Thr Pro Leu Val Lys Leu Leu Thr Asn Ser Ile
           4795                4800                4805

ggt tta cct ccc cac aac ctc atg ctg gct acg gac cgt tat gac cgt   35427
Gly Leu Pro Pro His Asn Leu Met Leu Ala Thr Asp Arg Tyr Asp Arg
       4810                4815                4820

gat tct gaa cag caa att cgt caa caa gtc gca ttc agt gat ggt ttt   35475
Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly Phe
   4825                4830                4835

ggc cgt ttg ttg caa gcg gct gtg cgg cat gag gca ggc gaa gcc tgg   35523
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Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala Trp
4840                4845                4850                4855

caa cgt aac caa gac ggt tct ctg gtg aca aaa atg gaa gat acc aaa   35571
Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr Lys
                4860                4865                4870

acg cgc tgg gcg att acg gga cgc act gaa tat gac aat aag ggg cag   35619
Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly Gln
            4875                4880                4885

gcg ata cga act tat cag ccc tat ttc ctc aat gac tgg cga tat gtg   35667
Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr Val
        4890                4895                4900

agt gat gac agc gcc aga aaa gag gcc tat gcc gat act cat atc tat   35715
Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile Tyr
    4905                4910                4915

gat ccg att ggg cgg gaa atc caa gtt atc acg gca aaa ggc tgg ctg   35763
Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp Leu
4920                4925                4930                4935

cgg cag aac caa tat ttc ccg tgg ttt acc gtg agt gaa gat gaa aat   35811
Arg Gln Asn Gln Tyr Phe Pro Trp Phe Thr Val Ser Glu Asp Glu Asn
                4940                4945                4950

gat ttg tcc gct gac gcg ctc gtg taa ttgaatcaag attcgctcgt         35858
Asp Leu Ser Ala Asp Ala Leu Val
            4955                4960

ttaatgttaa cgagcgaata taatatacct aatagatttc gagttgcagc gcggcggcaa 35918

gtgaacgaat ccccaggagc atagataact atgtgactgg ggtgagtgaa agcagccaac 35978

aaagcagcag cttgaaagat gaagggtata aataagaaac tgcattgtga gttctaaata 36038

gagtagcagc atattttatt gccttttatt tcataggtaa taaaattcaa ttgctgtaaa 36098

aatctgtcat catgagaact aaaaataaca actttctctt ctgcaagaga aatcaataat 36158

tcaattaaaa atgttataga atctgaatca agaccatttg ttggctcatc aaaaatataa 36218

acatccgcat cggtaataaa agctgatgtc aatagaaatt tctttttttat cccaagtgac 36278

atatgtccat actcaatacc agaataatta gatataccaa aaccatttaa atagtaatct 36338

aattgatatt ttaaattact tttcctataa cgctgactta aattaatcac atccattccc 36398

gtgatgaaat tataaaagtt aacattatcc gatagataaa aaccatgctg ttgcaaatta 36458

aatcggctct tttctccctt ttttataaaa ttaaccattc ctttttttaac cttatttaca 36518

ccagcaatac ttgaaagaaa agtcgtttta cccgccccat taactcccgc aatacggttt 36578

aatccaaccc gaaaatcaca attgactcct gaaaaaatag tcttaccatt aataacaacc 36638

tctaacccaa taacttcaag cataaataac ccctaaaaat aacgtaaaaa agaaaataac 36698

accaacaata ataattttcg tgtattgcgt tctcaacaga gaaatagaag aaacaataat 36758

agaaagaaaa gcataagata aaaatataat cacaggaaaa gatttaacaa caagaaagca 36818

aaaaataaaa aaacaaagca aataaaaaaa caaagaaata ccataattaa aaaagaatat 36878
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tttccgcaca gataaaaagt tggacaaata tgaaagataa tttatttcaa tatatgatag 36938

attataaaat aacaacatgc atatatataa aacaacactg gcatatatta atgatatata 36998

atcagccttg tttgggattt gagaaaaggc actttcacat aatagatata aaagcagaac 37058

agataatgcc ataataagca cagacatttt atttttatta aaacaataac gaagattcat 37118

tatataaggc aatgaaaaaa aacctgatga aaataatttt ttatttctat taattatata 37178

acatggtgtg aaattcaaat ataatatcaa tgctactaat ggaataacta atgtaaaaat 37238

caaatcatat aatattccac tcctgaatga tgccgccaga agaaagaaca cagcaacaat 37298

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caaaaaaaac acagatgaaa ggtaatgcaa ataattaaca ttttcgtaaa aaaaacctat 37418

aaagaagaaa ataactatcg gaaaagcact ataaataaaa aaaacgatac gactaaaaaa 37478

caacgttttt ttacctacca aagaaacgat gattgaattc tcctttgcag aaggaaaaaa 37538

ccttatgtta atcaaataaa ataccatata taccattaaa gatatggcag taaaataaaa 37598

tgattttatg tagccatctg gaataataat attggaagat aaagttatta aaacctcaaa 37658

gataccactg aactttgccg gaagtaataa aagaaaaagg aatataatga catttttatt 37718

cccagacgca aatttcttta tcctaccttt atattccaag gcatcagcga ttattaaatt 37778

catactgcct ctctaaaacc aaaatctaaa taatgtcctt ggtgaatctt tagggaattt 37838

cgtcctggaa tgcaaatata aatagttact gaaaacaata cattgatttt taattaaata 37898

ctggcgatat gaccttaatg atgctacttt attttccagt attcaattcg 37948

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<212> PRT
<213> Photorhabdus luminescens

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Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln Lys Thr Pro Val Val Asn
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Ile Tyr Asp Asn Arg Gly Leu Thr Ile Arg Asn Ile Asp Phe His Arg
             20                  25                  30

Thr Thr Ala Asn Gly Asp Thr Asp Ile Arg Ile Thr Arg His Gln Tyr
         35                  40                  45

Asp Ser Leu Gly His Leu Ser Gln Ser Thr Asp Pro Arg Leu Tyr Glu
     50                  55                  60

Ala Lys Gln Lys Ser Asn Phe Leu Trp Gln Tyr Asp Leu Thr Gly Asn
 65                  70                  75                  80

Ile Leu Cys Thr Glu Ser Val Asp Ala Gly Arg Thr Val Thr Leu Asn
                 85                  90                  95

Asp Ile Glu Gly Arg Pro Leu Leu Thr Val Thr Ala Thr Gly Val Ile
            100                 105                 110

Gln Thr Arg Gln Tyr Glu Thr Ser Ser Leu Pro Gly Arg Leu Leu Ser
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        115                 120                 125

Val Thr Glu Gln Ile Pro Glu Lys Thr Ser Arg Ile Thr Glu Arg Leu
    130                 135                 140

Ile Trp Ala Gly Asn Ser Glu Ala Glu Lys Asn His Asn Leu Ala Ser
145                 150                 155                 160

Gln Cys Val Arg His Tyr Asp Thr Ala Gly Val Thr Arg Leu Glu Ser
                165                 170                 175

Leu Ser Leu Thr Gly Thr Val Leu Ser Gln Ser Ser Gln Leu Leu Ser
            180                 185                 190

Asp Thr Gln Glu Ala Ser Trp Thr Gly Asp Asn Glu Thr Val Trp Gln
        195                 200                 205

Asn Met Leu Ala Asp Asp Ile Tyr Thr Thr Leu Ser Ala Phe Asp Ala
    210                 215                 220

Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly Asn Ile Gln Arg
225                 230                 235                 240

Leu Thr Tyr Asp Val Ala Gly Gln Leu Asn Gly Ser Trp Leu Thr Leu
                245                 250                 255

Lys Asp Gln Pro Glu Gln Val Ile Ile Arg Ser Leu Thr Tyr Ser Ala
            260                 265                 270

Ala Gly Gln Lys Leu Arg Glu Glu His Gly Asn Gly Val Ile Thr Glu
        275                 280                 285

Tyr Ser Tyr Glu Pro Glu Thr Gln Gln Leu Ile Gly Thr Lys Thr His
    290                 295                 300

Arg Pro Ser Asp Ala Lys Val Leu Gln Asp Leu Arg Tyr Glu Tyr Asp
305                 310                 315                 320

Pro Val Gly Asn Val Ile Ser Ile Arg Asn Asp Ala Glu Ala Thr Arg
                325                 330                 335

Phe Trp His Asn Gln Lys Val Ala Pro Glu Asn Thr Tyr Thr Tyr Asp
            340                 345                 350

Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu Met Ala Asn Ile
        355                 360                 365

Gly Gln Gln Ser Asn Gln Leu Pro Ser Leu Thr Leu Pro Ser Asp Asn
    370                 375                 380

Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr Asp Arg Gly Gly
385                 390                 395                 400

Asn Leu Thr Lys Ile Gln His Ser Ser Pro Ala Thr Gln Asn Asn Tyr
                405                 410                 415

Thr Thr Asn Ile Thr Val Ser Asn Arg Ser Asn Arg Ala Val Leu Ser
            420                 425                 430

Thr Leu Thr Glu Asp Pro Ala Gln Val Asp Ala Leu Phe Asp Ala Gly
        435                 440                 445

Gly His Gln Asn Thr Leu Ile Ser Gly Gln Asn Leu Asn Trp Asn Thr
    450                 455                 460
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Arg Gly Glu Leu Gln His Val Thr Leu Val Lys Arg Asp Lys Gly Ala
465                 470                 475                 480

Asn Asp Asp Arg Glu Trp Tyr Arg Tyr Ser Ser Asp Gly Arg Arg Ile
                485                 490                 495

Leu Lys Ile Asn Glu Gln Gln Thr Ser Ser Asn Ser Gln Thr Gln Arg
            500                 505                 510

Ile Thr Tyr Leu Pro Ser Leu Glu Leu Arg Leu Thr Gln Asn Ser Thr
        515                 520                 525

Ile Thr Thr Glu Asp Leu Gln Val Ile Thr Val Gly Glu Ala Gly Arg
    530                 535                 540

Ala Gln Val Arg Val Leu His Trp Asp Ser Gly Gln Pro Glu Asp Ile
545                 550                 555                 560

Asp Asn Asn Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser
                565                 570                 575

Gln Leu Glu Leu Asp Ser Lys Gly Glu Ile Ile Ser Glu Glu Glu Tyr
            580                 585                 590

Tyr Pro Tyr Gly Gly Thr Ala Leu Trp Ala Thr Arg Lys Arg Thr Glu
        595                 600                 605

Ala Ser Tyr Lys Thr Ile Arg Tyr Ser Gly Lys Glu Arg Asp Ala Thr
    610                 615                 620

Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr Gln Pro Trp Val Gly Arg
625                 630                 635                 640

Trp Leu Ser Ala Asp Pro Ala Gly Thr Val Asp Gly Leu Asn Leu Tyr
                645                 650                 655

Arg Met Val Arg Asn Asn Pro Val Thr Leu Leu Asp Pro Asp Gly Leu
            660                 665                 670

Met Pro Thr Ile Ala Glu Arg Ile Ala Ala Leu Gln Lys Asn Lys Val
        675                 680                 685

Ala Asp Ser Ala Pro Ser Pro Thr Asn Ala Thr Asn Val Ala Ile Asn
    690                 695                 700

Ile Arg Pro Pro Val Ala Pro Lys Pro Thr Leu Pro Lys Ala Ser Thr
705                 710                 715                 720

Ser Ser Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro
                725                 730                 735

Thr Thr Ser Gly Ser Ser Ile Thr Ala Pro Leu Ser Pro Val Gly Asn
            740                 745                 750

Lys Ser Thr Pro Glu Ile Ser Leu Pro Glu Ser Thr Gln Ser Asn Ser
        755                 760                 765

Ser Ser Ala Ile Ser Thr Asn Leu Gln Lys Lys Ser Phe Thr Leu Tyr
    770                 775                 780

Arg Ala Asp Asn Arg Ser Phe Glu Asp Met Gln Ser Lys Phe Pro Glu
785                 790                 795                 800

Gly Phe Lys Ala Trp Thr Pro Leu Asp Thr Lys Met Ala Arg Gln Phe
                805                 810                 815
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Ala Ser Val Phe Ile Gly Gln Lys Asp Thr Ser Asn Leu Pro Lys Glu
820 825 830

Thr Val Lys Asn Ile Asn Thr Trp Gly Thr Lys Pro Lys Leu Asn Asp
835 840 845

Leu Ser Thr Tyr Ile Lys Tyr Thr Lys Asp Lys Ser Thr Val Trp Val
850 855 860

Ser Thr Ala Ile Asn Thr Glu Ala Gly Gly Gln Ser Ser Gly Ala Pro
865 870 875 880

Leu His Glu Ile Asn Met Asp Leu Tyr Glu Phe Thr Ile Asp Gly Gln
885 890 895

Lys Leu Asn Pro Leu Pro Arg Gly Arg Ser Lys Asp Arg Val Pro Ser
900 905 910

Leu Leu Leu Asp Thr Pro Glu Ile Glu Thr Ala Ser Ile Ile Ala Leu
915 920 925

Asn His Gly Pro Val Asn Asp Ala Glu Val Ser Phe Leu Thr Thr Ile
930 935 940

Pro Leu Lys Asn Val Lys Pro Tyr Lys Arg
945 950

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Asp Val Leu Lys Ile Gln Cys Gly Phe Gln Cys Leu Thr Asp Ile Ser
20 25 30

His Ser Ser Phe Asn Glu Phe His Gln Gln Val Ser Glu His Leu Ser
35 40 45

Trp Ser Glu Ala His Asp Leu Tyr His Asp Ala Gln Gln Ala Gln Lys
50 55 60

Asp Asn Arg Leu Tyr Glu Ala Arg Ile Leu Lys Arg Thr Asn Pro Gln
65 70 75 80

Leu Gln Asn Ala Val His Leu Ala Ile Val Ala Pro Asn Ala Glu Leu
85 90 95

Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val Ala
100 105 110

Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr Glu
115 120 125

Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr Arg
130 135 140

Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln Gln
145 150 155 160

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Asn Met Asp Thr Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu Leu
                165                 170                 175

Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Asp Asn Tyr Thr Gln Val
            180                 185                 190

Met Glu Met Leu Ser Ala Phe Arg Pro Ser Gly Ala Thr Pro Tyr His
        195                 200                 205

Asp Ala Tyr Glu Asn Val Arg Lys Val Ile Gln Leu Gln Asp Pro Gly
    210                 215                 220

Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His Gln
225                 230                 235                 240

Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe Asn
                245                 250                 255

Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr Lys
            260                 265                 270

Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu Tyr
        275                 280                 285

Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe Ile
    290                 295                 300

Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln Leu
305                 310                 315                 320

Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys Val Tyr Arg
                325                 330                 335

Ile Thr Arg Glu Tyr Thr Thr Asn Ala Asn Gln Val Asp Val Glu Leu
            340                 345                 350

Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys Phe Lys Asp
        355                 360                 365

Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg
    370                 375                 380

Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser
385                 390                 395                 400

Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro Phe Glu Ile
                405                 410                 415

Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr Ala Ala Ala
            420                 425                 430

Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu
        435                 440                 445

Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile
    450                 455                 460

Leu Glu Ser Ile Val Arg Ser Val Asn Gln Gln Leu Asp Ile Asn Ala
465                 470                 475                 480

Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr
                485                 490                 495

Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Leu Ile Ser
            500                 505                 510
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Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn
515 520 525

Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile
530 535 540

Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser Val Leu Lys
545 550 555 560

Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu Leu Lys Ile
565 570 575

Thr Asn His Asn Asn Gln Asp Gly Lys Ile Lys Asn Asn Leu Asn Asn
580 585 590

Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile His Gln Leu
595 600 605

Thr Ile Asp Glu Leu Asp Leu Leu Leu Val Ala Val Gly Glu Gly Glu
610 615 620

Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala Leu Ile Arg
625 630 635 640

Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys Trp Ser Ala
645 650 655

Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
660 665 670

Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
675 680 685

Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala Pro Tyr Ile
690 695 700

Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu
705 710 715 720

Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met Thr Ala Glu
725 730 735

Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp Ser Ser Glu
740 745 750

Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala
755 760 765

Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe
770 775 780

Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser Thr Glu Ala
785 790 795 800

Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala
805 810 815

Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala
820 825 830

Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn
835 840 845

Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala Gln Asn His

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    850                 855                 860

Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser Cys Trp Thr
865                 870                 875                 880

Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Asn
                885                 890                 895

Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp Tyr Ile Gln
            900                 905                 910

Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser Ala Gly Glu
        915                 920                 925

Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile Leu His Ala
    930                 935                 940

Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg
945                 950                 955                 960

Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr
                965                 970                 975

Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr
            980                 985                 990

Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Thr
        995                1000                1005

Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile Ser Arg Gln
   1010                1015                1020

Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala
025                1030                1035                1040

Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr
               1045                1050                1055

Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val
           1060                1065                1070

Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser
       1075                1080                1085

Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala
   1090                1095                1100

Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly
105                1110                1115                1120

Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser Val Asp His
               1125                1130                1135

Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
           1140                1145                1150

His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr Ile Arg Pro
       1155                1160                1165

Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
   1170                1175                1180

Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
185                1190                1195                1200
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Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
1205 1210 1215

Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile Ser Lys Leu
1220 1225 1230

Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
1235 1240 1245

Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
1250 1255 1260

Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
265 1270 1275 1280

Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser Tyr Arg Asp
1285 1290 1295

Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg Val Asn Asn
1300 1305 1310

Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn Ser Arg Lys
1315 1320 1325

Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
1330 1335 1340

Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu Lys Ile Tyr
345 1350 1355 1360

Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Gln
1365 1370 1375

Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
1380 1385 1390

Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
1395 1400 1405

Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn Val Ser Gly
1410 1415 1420

Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn Tyr Ser Ser
425 1430 1435 1440

Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu Thr Asn Pro
1445 1450 1455

Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro
1460 1465 1470

Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys Gly Thr Ala
1475 1480 1485

Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile Ser Pro Ala
1490 1495 1500

Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln Thr Phe Thr
505 1510 1515 1520

Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met
1525 1530 1535

Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser Leu Asn Phe
1540 1545 1550

Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala Phe Ala Glu
1555 1560 1565

Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Ile Thr Arg
1570 1575 1580

Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn Glu Asn Gly
585 1590 1595 1600

Ala Gln Tyr Met Gln Trp Gly Val Tyr Arg Ile Arg Leu Asn Thr Leu
1605 1610 1615

Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile
1620 1625 1630

Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly
1635 1640 1645

Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser Thr His Gly
1650 1655 1660

Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn
665 1670 1675 1680

Ser His Ile Ile Tyr Ser Gly Gln Leu Lys Asp Thr Asn Ile Ser Thr
1685 1690 1695

Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr Ser
1700 1705 1710

Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp
1715 1720 1725

Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn
1730 1735 1740

Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn
745 1750 1755 1760

Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe
1765 1770 1775

Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu
1780 1785 1790

His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp
1795 1800 1805

Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp
1810 1815 1820

Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu
825 1830 1835 1840

Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr
1845 1850 1855

Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly
1860 1865 1870

Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys
1875 1880 1885

Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu

1890 1895 1900

Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys Ala Ala Asp
905 1910 1915 1920

Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala Leu Arg Gln
1925 1930 1935

Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr Leu Thr Asp
1940 1945 1950

Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr Trp Gln Thr
1955 1960 1965

Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser Ile Asp Gly
1970 1975 1980

Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp Pro Lys Ala
985 1990 1995 2000

Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly Lys Leu Pro
2005 2010 2015

Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu Glu Asn Ala
2020 2025 2030

Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr Leu Gln Asn
2035 2040 2045

Ile Ile Glu Arg Gln Asp Ala Glu Ala Leu Asn Ala Leu Leu Gln Asn
2050 2055 2060

Gln Ala Ala Glu Leu Ile Leu Thr Asn Leu Ser Ile Gln Asp Lys Thr
065 2070 2075 2080

Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys Ser Lys Ala
2085 2090 2095

Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His Asp Glu Asn
2100 2105 2110

Ile Asn Ala Gly Glu Asn Gln Ala Met Thr Leu Arg Ala Ser Ala Ala
2115 2120 2125

Gly Leu Thr Thr Ala Val Gln Ala Ser Arg Leu Ala Gly Ala Ala Ala
2130 2135 2140

Asp Leu Val Pro Asn Ile Phe Gly Phe Ala Gly Gly Gly Ser Arg Trp
145 2150 2155 2160

Gly Ala Ile Ala Glu Ala Thr Gly Tyr Val Met Glu Phe Ser Ala Asn
2165 2170 2175

Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu Thr Tyr Arg
2180 2185 2190

Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala Glu Ala Glu
2195 2200 2205

Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val Arg Arg Glu
2210 2215 2220

Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln Glu Gln Thr
225 2230 2235 2240

Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn Gln Ala Leu
2245 2250 2255

Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Phe Gln Phe Tyr
2260 2265 2270

Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp
2275 2280 2285

Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln
2290 2295 2300

Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met Leu Ser Leu
305 2310 2315 2320

Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg Ala Leu Glu
2325 2330 2335

Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly Leu Pro Gln
2340 2345 2350

Asp Lys Gly Pro Phe Ser Leu Thr Gln Glu Ile Glu Lys Leu Val Asn
2355 2360 2365

Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly
2370 2375 2380

Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile Ser Leu Ala
385 2390 2395 2400

Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly Lys Ile Arg
2405 2410 2415

Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr
2420 2425 2430

Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala
2435 2440 2445

Asn Gly Cys Ala Ala Leu Ala Val Ser His Gly Thr Asn Asp Ser Gly
2450 2455 2460

Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Phe Leu Pro Phe Glu Gly
465 2470 2475 2480

Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser
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Ile Ile Leu His Ile Arg Tyr Thr Ile Lys
2515 2520

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Pro Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly
         35                  40                  45

Arg Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly
     50                  55                  60

Asn Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg
 65                  70                  75                  80

Arg Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe
                 85                  90                  95

Leu Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly
            100                 105                 110

Gln Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly
        115                 120                 125

Met Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe
    130                 135                 140

Ser Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe
145                 150                 155                 160

Trp Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn
                165                 170                 175

Pro Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln
            180                 185                 190

Trp Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr
        195                 200                 205

Gln Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr
    210                 215                 220

Ala His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr
225                 230                 235                 240

Gly Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp
                245                 250                 255

Pro Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu
            260                 265                 270

Arg Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn
        275                 280                 285

Trp Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala
    290                 295                 300

Leu Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu
305                 310                 315                 320

Gln Thr Leu Ser Gly Gln Ala Lys Gly Asp Asp Glu Pro Ala Leu Val
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Ser Arg Leu Ile Leu Asp Tyr Asp Glu Asn Ala Val Val Ser Thr Leu
            340                 345                 350

Val Ser Val Arg Arg Val Gly His Glu Gln Asp Gly Thr Thr Ala Val
        355                 360                 365
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Ala Leu Pro Pro Leu Glu Leu Ala Tyr Gln Pro Phe Glu Pro Glu Gln
370 375 380

Lys Ala Leu Trp Arg Pro Met Asp Val Leu Ala Asn Phe Asn Thr Ile
385 390 395 400

Gln Arg Trp Gln Leu Leu Asp Leu Gln Gly Glu Gly Val Pro Gly Ile
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Leu Tyr Gln Asp Lys Asn Gly Trp Trp Tyr Arg Ser Ala Gln Arg Gln
420 425 430

Thr Gly Glu Glu Met Asn Ala Val Thr Trp Gly Lys Met Gln Leu Leu
435 440 445

Pro Ile Thr Pro Ala Ile Gln Asp Asn Ala Ser Leu Met Asp Ile Asn
450 455 460

Gly Asp Gly Gln Leu Asp Trp Val Ile Thr Gly Pro Gly Leu Arg Gly
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Tyr His Ser Gln His Pro Asp Gly Ser Trp Thr Arg Phe Thr Pro Leu
485 490 495

His Ala Leu Pro Ile Glu Tyr Thr His Pro Arg Ala Gln Leu Ala Asp
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Leu Met Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro Lys Ser
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Val Arg Leu Tyr Ala Asn Asn Arg Asp Gly Phe Thr Glu Gly Arg Asp
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Val Val Gln Ser Gly Gly Ile Thr Leu Pro Leu Pro Gly Ala Asp Ala
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Arg Lys Leu Val Ala Phe Ser Asp Val Leu Gly Ser Gly Gln Ala His
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Leu Val Glu Val Ser Ala Thr Lys Val Thr Cys Trp Pro Asn Leu Gly
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His Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser
595 600 605

Ala Ala Asn Phe Asn Pro Asp Arg Val His Leu Ala Asp Leu Asp Gly
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Ser Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile
625 630 635 640

Phe Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg
645 650 655

Phe Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala
660 665 670

Asp Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His
675 680 685

Met Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp
690 695 700

Leu Leu Ser Glu Met Asn Asn Asn Met Gly Ala His His Thr Leu His
705 710 715 720

Tyr Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu
725 730 735

Ala Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr
740 745 750

Leu Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val
755 760 765

Thr Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu
770 775 780

Phe Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Gln Leu Ala
785 790 795 800

Gln Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp
805 810 815

Tyr Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr
820 825 830

Trp Arg Gly Asp Thr Gln Ala Phe Thr Gly Phe Thr Pro His Phe Thr
835 840 845

Leu Trp Lys Glu Gly Lys Asp Val Pro Leu Thr Pro Glu Asp Asp His
850 855 860

Asn Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser
865 870 875 880

Glu Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr
885 890 895

Val Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr
900 905 910

Leu Ser Pro Val Leu Trp Ala Ser Val Val Glu Ser Arg Ser Tyr His
915 920 925

Tyr Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu
930 935 940

Ser Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr
945 950 955 960

Pro Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro
965 970 975

Asp Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg
980 985 990

Leu Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu
995 1000 1005

Arg Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr
1010 1015 1020

Asp Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys
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Ala Glu Asn Ser Leu Ile Ala Asp Asp Lys Pro Arg Glu Tyr Leu Asn
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Gln Gln Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro

1060 1065 1070

Thr Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu
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Thr Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Phe Asp Gly Gly Ile
1090 1095 1100

Thr Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln
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Glu Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala
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Arg Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro
1140 1145 1150

Val Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp
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Asp Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu
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Thr Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu
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Thr Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly
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Arg Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr
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Gly Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val
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Val Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe
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Arg Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly
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Phe Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala
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Trp Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr
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Lys Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly
1395 1400 1405

Gln Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr
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Val Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile
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Tyr Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp
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cgggatttat catgatatta tggccgaatg tgatgtgaac aattatttta taattagatt 180

aataatataa tggtattaaa atagcaatat atttatttct gggtatttat catcggtttt 240

attaaatggg gaatcaatcta taaattagtt ttacataatt cacaaatagc gattocatta 300

accoggaata ttaaaaatax ttatttatga ttatggtgat atatcttrat tagcctactt 360

ttataactag aaaaattgac attttcaatc catgtataaa tggtaaccaa t atg cag 417
Met Gln
1

agg gct caa cga gtt gtt att aca ggt atg ggt gcc gta aca ccg att 465
Arg Ala Gln Arg Val Val Ile Thr Gly Met Gly Ala Val Thr Pro Ile
5 10 15

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ggt gaa gat gtt gaa tca tgt tgg caa agt att att gaa aaa caa cat   513
Gly Glu Asp Val Glu Ser Cys Trp Gln Ser Ile Ile Glu Lys Gln His
     20                  25                  30

cga ttt cac aga att gaa ttt cct gac tca ttc att aat tcg cgt ttc   561
Arg Phe His Arg Ile Glu Phe Pro Asp Ser Phe Ile Asn Ser Arg Phe
 35                  40                  45                  50

ttt tct ttc ctt gca cca aac cca tcc cgc tat cag tta tta cca aaa   609
Phe Ser Phe Leu Ala Pro Asn Pro Ser Arg Tyr Gln Leu Leu Pro Lys
                 55                  60                  65

aag ttg act cat aca ctt tct gac tgc gga aaa gca gca ttg aag gcg   657
Lys Leu Thr His Thr Leu Ser Asp Cys Gly Lys Ala Ala Leu Lys Ala
             70                  75                  80

act tat caa gct ttt acc caa gca ttc ggc gtg aat ata tca cct gtt   705
Thr Tyr Gln Ala Phe Thr Gln Ala Phe Gly Val Asn Ile Ser Pro Val
         85                  90                  95

gaa tat tac gat aaa tac gaa tgt ggc gta att ctt ggc agt ggt tgg   753
Glu Tyr Tyr Asp Lys Tyr Glu Cys Gly Val Ile Leu Gly Ser Gly Trp
    100                 105                 110

ggc gct att gat aat gcc gga gat cat gct tgc caa tat aag caa gca   801
Gly Ala Ile Asp Asn Ala Gly Asp His Ala Cys Gln Tyr Lys Gln Ala
115                 120                 125                 130

aaa tta gct cat cct atg agt aat ctt att acc atg cca agc tcc atg   849
Lys Leu Ala His Pro Met Ser Asn Leu Ile Thr Met Pro Ser Ser Met
                135                 140                 145

acg gct gca tgt tcg att atg tat gga cta cgt ggt tat caa aat acc   897
Thr Ala Ala Cys Ser Ile Met Tyr Gly Leu Arg Gly Tyr Gln Asn Thr
            150                 155                 160

gtt atg gct gcc tgc gca acg ggc aca atg gcg ata ggc gat gcc ttt   945
Val Met Ala Ala Cys Ala Thr Gly Thr Met Ala Ile Gly Asp Ala Phe
        165                 170                 175

gaa att att cgc tca ggg cgg gca aaa tgt atg att gcc gga gcc gct   993
Glu Ile Ile Arg Ser Gly Arg Ala Lys Cys Met Ile Ala Gly Ala Ala
    180                 185                 190

gaa tca ctc acg cgg gaa tgt aat att tgg agt att gat gta ctg aat  1041
Glu Ser Leu Thr Arg Glu Cys Asn Ile Trp Ser Ile Asp Val Leu Asn
195                 200                 205                 210

gca tta tcg aaa gaa caa gcg gac cca aat ctt gca tgt tgt cca ttt  1089
Ala Leu Ser Lys Glu Gln Ala Asp Pro Asn Leu Ala Cys Cys Pro Phe
                215                 220                 225

agc ctt gat cgc tct gga ttt gta tta gcc gaa gga gcg gcg gta gtt  1137
Ser Leu Asp Arg Ser Gly Phe Val Leu Ala Glu Gly Ala Ala Val Val
            230                 235                 240

tgt ctg gaa aat tat gat tca gcc atc gcg cgt ggt gca acg att tta  1185
Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr Ile Leu
        245                 250                 255

gcg gaa att aaa ggt tac gcc caa tat tca gat gcc gtt aat tta acc  1233
Ala Glu Ile Lys Gly Tyr Ala Gln Tyr Ser Asp Ala Val Asn Leu Thr
    260                 265                 270
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cgg cca aca gaa gat att gaa cct aaa ata tta gcg ata act aaa gcc   1281
Arg Pro Thr Glu Asp Ile Glu Pro Lys Ile Leu Ala Ile Thr Lys Ala
275                 280                 285                 290

att gag cag gca cag att tcg ccg aaa gat att gac tac att aat gct   1329
Ile Glu Gln Ala Gln Ile Ser Pro Lys Asp Ile Asp Tyr Ile Asn Ala
                295                 300                 305

cat ggt act tct aca ccg tta aat gat ctt tat gaa act cag gca att   1377
His Gly Thr Ser Thr Pro Leu Asn Asp Leu Tyr Glu Thr Gln Ala Ile
            310                 315                 320

aaa gcg gca ctg ggc caa tat gct tat cag gta cct ata tca agc aca   1425
Lys Ala Ala Leu Gly Gln Tyr Ala Tyr Gln Val Pro Ile Ser Ser Thr
        325                 330                 335

aaa tct tat acc ggc cac ctt act gct gcc gcc ggt agt ttt gaa acg   1473
Lys Ser Tyr Thr Gly His Leu Ile Ala Ala Ala Gly Ser Phe Glu Thr
    340                 345                 350

att gta tgt gtg aaa gca tta gct gaa aat tgc ttg cca gca acc ttg   1521
Ile Val Cys Val Lys Ala Leu Ala Glu Asn Cys Leu Pro Ala Thr Leu
355                 360                 365                 370

aat tta cac cgg gct gat cca gat tgc gat ctc aat tat ttg cct aat   1569
Asn Leu His Arg Ala Asp Pro Asp Cys Asp Leu Asn Tyr Leu Pro Asn
                375                 380                 385

caa cat tgc tac acc gct caa cca gag gtg aca ctc aat att agc gca   1617
Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile Ser Ala
            390                 395                 400

ggt ttc ggc ggg cat aac gct gcg ttg gtt atc gct aag gta agg taa   1665
Gly Phe Gly Gly His Asn Ala Ala Leu Val Ile Ala Lys Val Arg
        405                 410                 415

ctgatatgtt gatttttgca atg gaa gat act gaa cat tgg tcg aat ttc tct 1718
                    Met Glu Asp Ile Glu His Trp Ser Asn Phe Ser
                420                 425

ggg gat ttt aac ccc atc cat tat tcg gcg aaa agt gag tct ttg cgc   1766
Gly Asp Phe Asn Pro Ile His Tyr Ser Ala Lys Ser Glu Ser Leu Arg
430                 435                 440                 445

aat ata cag caa cac ccg gtg cag gga atg ttg agt ttg ctc tat gta   1814
Asn Ile Gln Gln His Pro Val Gln Gly Met Leu Ser Leu Leu Tyr Val
                450                 455                 460

cgg caa cag ttt tct caa tta act tcc gct ttt aca aag ggc ata ttg   1862
Arg Gln Gln Phe Ser Gln Leu Thr Ser Ala Phe Thr Thr Gly Ile Leu
            465                 470                 475

aac att gat gcc tct ttc cgc cag tat gtt tat acc gca tta ccc cat   1910
Asn Ile Asp Ala Ser Phe Arg Gln Tyr Val Tyr Thr Ala Leu Pro His
        480                 485                 490

caa ctg agg att aat act aaa aac aaa acg ttt aaa tta gaa aat ccc   1958
Gln Leu Arg Ile Asn Thr Lys Asn Lys Thr Phe Lys Leu Glu Asn Pro
    495                 500                 505

agt aaa gaa aac acg ttg ttc ggc aat acc agc gta gag aat aca atg   2006
Ser Lys Glu Asn Thr Leu Phe Gly Asn Thr Ser Val Glu Asn Thr Met
510                 515                 520                 525

gag tca att gaa gat tgg atc gtt cag gat aat tgt caa aaa cta acg   2054
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Glu Ser Ile Glu Asp Trp Ile Val Gln Asp Asn Cys Gln Lys Leu Thr
                530                 535                 540

ata aca ggg gag gaa gtt tgt gaa aag tat gct gtc ttt agg tac tat  2102
Ile Thr Gly Glu Glu Val Cys Glu Lys Tyr Ala Val Phe Arg Tyr Tyr
            545                 550                 555

ttc cca agt gtc act tct att gga tgg ttc ctg gat gcg ctt gct ttt  2150
Phe Pro Ser Val Thr Ser Ile Gly Trp Phe Leu Asp Ala Leu Ala Phe
        560                 565                 570

cat ctt att att aat tcg aca ggg ttt ctt aat ttt gag cac tac cat  2198
His Leu Ile Ile Asn Ser Thr Gly Phe Leu Asn Phe Glu His Tyr His
    575                 580                 585

ttt aac caa tta cag gat tat ctg agt caa tct ttt act ttg cat act  2246
Phe Asn Gln Leu Gln Asp Tyr Leu Ser Gln Ser Phe Thr Leu His Thr
590                 595                 600                 605

ggg caa gcg att aaa atc agg aag gag att gtt aat agt aca gta tta  2294
Gly Gln Ala Ile Lys Ile Arg Lys Glu Ile Val Asn Ser Thr Val Leu
                610                 615                 620

tta tct tca ccg gat atc tgt gtt gaa tta aat cct cct tta ttg att  2342
Leu Ser Ser Pro Asp Ile Cys Val Glu Leu Asn Pro Pro Leu Leu Ile
            625                 630                 635

aag aat ggc gat aaa gat tat att cgt att ttc tat tat cga tgt tta  2390
Lys Asn Gly Asp Lys Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu
        640                 645                 650

tat gat aaa aaa cct att ttt gta tca aag act tca att atc tct aag  2438
Tyr Asp Lys Lys Pro Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys
    655                 660                 665

atg aaa taa aaggaaagcg aaatgccaac acaaagtgat attttcactg          2487
Met Lys
670

aaataaagaa tagaatatta atgatgaagg atategaaga tgaagaaata acaaaagagt 2547

cctcttttgt ttcgcttgaa tttgatagtc ttgactatgt ggaaatccaa gttttigtgt 2607

tggaagcgta tggtattgtg cttaaagccg aacttttttc aaatcattct atttcaacat 2667

taaatgagct cactgactat ttaaaatcaa aattgtaatc tgaattttta cttaaitaig 2727

ttttttcacc attaacatta agaggttata atg aac gtt tta gaa caa ggt aag  2781
                          Met Asn Val Leu Glu Gln Gly Lys
                                675                 680

gtt gct gct tta tat tca gcc tat tcg gaa aca gaa ggt tct tcg tgg  2829
Val Ala Ala Leu Tyr Ser Ala Tyr Ser Glu Thr Glu Gly Ser Ser Trp
            685                 690                 695

gtg gga aac ttg tgc tgt ttt tca agt gat cgg gag cat ttg cct att  2877
Val Gly Asn Leu Cys Cys Phe Ser Ser Asp Arg Glu His Leu Pro Ile
        700                 705                 710

atc gtg aat ggg cgt cgt ttc ttg att gaa ttt gtt att cca gat cat  2925
Ile Val Asn Gly Arg Arg Phe Leu Ile Glu Phe Val Ile Pro Asp His
    715                 720                 725

tta ctt gat gaa acg gtt aaa ccc aga gta ttc gat ttg gat atc aat  2973
Leu Leu Asp Lys Thr Val Lys Pro Arg Val Phe Asp Leu Asp Ile Asn
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    730                 735                 740

aaa caa ttt tta ctg cgt cgt gac cat cgt gag ata aat att tat ctt   3021
Lys Gln Phe Leu Leu Arg Arg Asp His Arg Glu Ile Asn Ile Tyr Leu
745                 750                 755                 760

tta ggt gaa gga aat ttt atg gat cgg acg acg aca gat aaa aat cta   3069
Leu Gly Glu Gly Asn Phe Met Asp Arg Thr Thr Thr Asp Lys Asn Leu
                765                 770                 775

ttc gag tta aat gag gat ggt tca cta ttt att aag acg tta cgc cat   3117
Phe Glu Leu Asn Glu Asp Gly Ser Leu Phe Ile Lys Thr Leu Arg His
            780                 785                 790

gct ctt ggt aaa tat gtt gct att aat cct tca act acg caa ttt atc   3165
Ala Leu Gly Lys Tyr Val Ala Ile Asn Pro Ser Thr Thr Gln Phe Ile
        795                 800                 805

ttc ttt gca caa gga aag tac agt gaa ttt atc atg aat gcc tta aag   3213
Phe Phe Ala Gln Gly Lys Tyr Ser Glu Phe Ile Met Asn Ala Leu Lys
    810                 815                 820

aca gtt gaa gac gaa tta tca aaa cgt tat cga gtc aga att att cct   3261
Thr Val Glu Asp Glu Leu Ser Lys Arg Tyr Arg Val Arg Ile Ile Pro
825                 830                 835                 840

gaa ttg caa ggg ccg tat tat ggc ttt gaa ctt gat att ctt tct att   3309
Glu Leu Gln Gly Pro Tyr Tyr Gly Phe Glu Leu Asp Ile Leu Ser Ile
                845                 850                 855

aca gct taa ttcacaatat tatggaggcgt gtt atg gaa aag aaa ata aca aca 3362
Thr Ala                             Met Glu Lys Lys Ile Thr Thr
                                    860                 865

ttt acc att gag aaa act gat gac aat ttt tat gct aat ggg cgt cat   3410
Phe Thr Ile Glu Lys Thr Asp Asp Asn Phe Tyr Ala Asn Gly Arg His
            870                 875                 880

caa tgt atg gta aaa atc tct gta ctt aaa caa gaa tat agg aat ggt   3458
Gln Cys Met Val Lys Ile Ser Val Leu Lys Gln Glu Tyr Arg Asn Gly
        885                 890                 895

gat tgg ata aaa cta gca ctt agt gag gct gaa aca aga tcg att cag   3506
Asp Trp Ile Lys Leu Ala Leu Ser Glu Ala Glu Lys Arg Ser Ile Gln
    900                 905                 910

gtg gcg gca tta agt gat agc ctc ata tat gac caa tta aaa atg cct   3554
Val Ala Ala Leu Ser Asp Ser Leu Ile Tyr Asp Gln Leu Lys Met Pro
915                 920                 925                 930

tca ggt tgg aca acg aca gat gca aga aat aaa ttt gat ctt ggg tta   3602
Ser Gly Trp Thr Thr Thr Asp Ala Arg Asn Lys Phe Asp Leu Gly Leu
                935                 940                 945

tta aat ggt gtt tat cat gct gat gct ttt atc gac gaa cag gta aac   3650
Leu Asn Gly Val Tyr His Ala Asp Ala Phe Ile Asp Glu Gln Val Thr
            950                 955                 960

gat cgt gcg gga gat tgc tgc aca aat gaa aac tat cag aac agt gtg   3698
Asp Arg Ala Gly Asp Cys Cys Thr Asn Glu Asn Tyr Gln Asn Ser Val
        965                 970                 975

aaa agt gtt cct gaa att atc tat cgt tat gtc agt agt aat aga aca   3746
Lys Ser Val Pro Glu Ile Ile Tyr Arg Tyr Val Ser Ser Asn Arg Thr
    980                 985                 990
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agc aca gaa tac cta atg gca aaa atg acc ttt gaa gat acg gat ggg  3794
Ser Thr Glu Tyr Leu Met Ala Lys Met Thr Phe Glu Asp Thr Asp Gly
995                1000                1005                1010

aaa cgc aca tta aca acg aat atg tca gtt ggt gat gaa gtt ttt gac  3842
Lys Arg Thr Leu Thr Thr Asn Met Ser Val Gly Asp Glu Val Phe Asp
               1015                1020                1025

agc aag gtt tta tta aaa gcc att gct cct tat gca att aat aca aat  3890
Ser Lys Val Leu Leu Lys Ala Ile Ala Pro Tyr Ala Ile Asn Thr Asn
          1030                1035                1040

caa ttg cat gaa aac atc aat aga ttg ttt gat aaa aca gaa gag ccg  3938
Gln Leu His Glu Asn Ile Asn Thr Leu Phe Asp Lys Thr Glu Glu Pro
     1045                1050                1055

aca aaa tcc gat act cat cat caa ata att aat ctt tat cgc tgg aca  3986
Thr Lys Ser Asp Thr His His Gln Ile Ile Asn Leu Tyr Arg Trp Thr
1060                1065                1070

ttg cca tat cat tta agg att ctt gaa ggg aat gac agt act gtt aat  4034
Leu Pro Tyr His Leu Arg Ile Leu Glu Gly Asn Asp Ser Thr Val Asn
1075                1080                1085                1090

aga ata tat gtc ctt ggt aaa gag cca tca aat gat aga ttc ctg aca  4082
Arg Ile Tyr Val Leu Gly Lys Glu Pro Ser Asn Asp Arg Phe Leu Thr
               1095                1100                1105

aga gga aag gta ttt aaa cga gga act cat atg tga atgcacgtga       4128
Arg Gly Arg Val Phe Lys Arg Gly Thr His Met
          1110                1115

taatgtgagt ggaggatgtg ttattggcct tccttatacc gtaactattc cggacacgca 4188

gcttgctgct gaagtgcttc atgtgacagg gtgttcgtgg ccgagtggtt attatgatgg 4248

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aaataggaat atagccatat ctgtaattat acatttaacga attttttactc gaatataatt 4488

ttaattgatc aaacaggaaa tttaaa atg aaa gct acc gat ata tat tcc aat  4541
                          Met Lys Ala Thr Asp Ile Tyr Ser Asn
                             1120                1125

gct ttt aat ttc ggt tct tat att aat act ggt gtc gat ccc aga acc  4589
Ala Phe Asn Phe Gly Ser Tyr Ile Asn Thr Gly Val Asp Pro Arg Thr
     1130                1135                1140

ggt caa tat agt gca aat att aat att atc acg tta aga cct aat aat  4637
Gly Gln Tyr Ser Ala Asn Ile Asn Ile Ile Thr Leu Arg Pro Asn Asn
1145                1150                1155

gtg ggt aat tcg gaa caa acg ttg agc cta tca ttc tcg cca tta aca  4685
Val Gly Asn Ser Glu Gln Thr Leu Ser Leu Ser Phe Ser Pro Leu Thr
1160                1165                1170                1175

acg tta aac aat ggc ttt ggt att ggc tgg cgc ttt tca tta aca aca  4733
Thr Leu Asn Asn Gly Phe Gly Ile Gly Trp Arg Phe Ser Leu Thr Thr
               1180                1185                1190
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tta gat ata aaa aca ctt aca ttt agc cga gca aat ggg gag caa ttt   4781
Leu Asp Ile Lys Thr Leu Thr Phe Ser Arg Ala Asn Gly Glu Gln Phe
          1195                1200                1205

aaa tgt aag cca ttg ccg cct aat aat aat gat ctt agt ttt aaa gat   4829
Lys Cys Lys Pro Leu Pro Pro Asn Asn Asn Asp Leu Ser Phe Lys Asp
       1210                1215                1220

aaa aaa cta aaa gat ttg cgc gta tat aag ctc gat agc aat act ttt   4877
Lys Lys Leu Lys Asp Leu Arg Val Tyr Lys Leu Asp Ser Asn Thr Phe
   1225                1230                1235

tat gtt tat aac aaa aac ggc att ata gag ata ctt aaa cgg att ggg   4925
Tyr Val Tyr Asn Lys Asn Gly Ile Ile Glu Ile Leu Lys Arg Ile Gly
1240                1245                1250                1255

tcg agt gat att gca aaa aca gtt gca ctt gaa ttt cct gat ggt gaa   4973
Ser Ser Asp Ile Ala Lys Thr Val Ala Leu Glu Phe Pro Asp Gly Glu
               1260                1265                1270

gca ttt gat tta att tat aat tca aga ttt gca ttg tcc gaa ata aaa   5021
Ala Phe Asp Leu Ile Tyr Asn Ser Arg Phe Ala Leu Ser Glu Ile Lys
          1275                1280                1285

tac cgt gtg aca ggt aaa act tat ctt aaa ctc aat tac tct gga aat   5069
Tyr Arg Val Thr Gly Lys Thr Tyr Leu Lys Leu Asn Tyr Ser Gly Asn
       1290                1295                1300

aac tgt aca tca gtg gaa tac cct gat gat aat aat att tct gcg aaa   5117
Asn Cys Thr Ser Val Glu Tyr Pro Asp Asp Asn Asn Ile Ser Ala Lys
   1305                1310                1315

ata gca ttc gat tat cgt aac gat tac ctt att acg gtg act gta cct   5165
Ile Ala Phe Asp Tyr Arg Asn Asp Tyr Leu Ile Thr Val Thr Val Pro
1320                1325                1330                1335

tac gat gct tct ggt cct att gat tct gcc cga ttt aag atg acc tat   5213
Tyr Asp Ala Ser Gly Pro Ile Asp Ser Ala Arg Phe Lys Met Thr Tyr
               1340                1345                1350

cag aca tta aaa ggc gta ttt cca gtt atc agc aac ttc cgt aca cca   5261
Gln Thr Leu Lys Gly Val Phe Pro Val Ile Ser Thr Phe Arg Thr Pro
          1355                1360                1365

acc ggt tat gtt gag ctg gtg agt tat aaa gag aat ggg cat aaa gtg   5309
Thr Gly Tyr Val Glu Leu Val Ser Tyr Lys Glu Asn Gly His Lys Val
       1370                1375                1380

acg gac acg gaa tat att cct tat gcg gct gca ctc act att caa ccc   5357
Thr Asp Thr Glu Tyr Ile Pro Tyr Ala Ala Ala Leu Thr Ile Gln Pro
   1385                1390                1395

ggc aat gga caa cct gcg gtc agc aaa tcc tat gaa tat agt tca gta   5405
Gly Asn Gly Gln Pro Ala Val Ser Lys Ser Tyr Glu Tyr Ser Ser Val
1400                1405                1410                1415

cat aac ttc ttg ggc tat tct tct ggt cgg aca agc ttt gat tcc agt   5453
His Asn Phe Leu Gly Tyr Ser Ser Gly Arg Thr Ser Phe Asp Ser Ser
               1420                1425                1430

caa gat aat ttg tat ttg gtc aca ggg aaa tac act tat tca tcc att   5501
Gln Asp Asn Leu Tyr Leu Val Thr Gly Lys Tyr Thr Tyr Ser Ser Ile
          1435                1440                1445

gaa cgg gtt tta gat ggt caa agt gtg gtt tca gta ata gaa cga gta   5549
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Glu Arg Val Leu Asp Gly Gln Ser Val Val Ser Val Ile Glu Arg Val
      1450                1455                1460

ttt aat aaa ttc cat tta atg acc aaa gaa gca aaa aca caa gat aat   5597
Phe Asn Lys Phe His Leu Met Thr Lys Glu Ala Lys Thr Gln Asp Asn
   1465                1470                1475

aag aga att acc aca gaa att act tac aat gag gat cta tca aaa agt   5645
Lys Arg Ile Thr Thr Glu Ile Thr Tyr Asn Glu Asp Leu Ser Lys Ser
1480                1485                1490                1495

ttc tca gag caa cca gaa aat tta caa caa cct tct cgc gtg tta acc   5693
Phe Ser Glu Gln Pro Glu Asn Leu Gln Gln Pro Ser Arg Val Leu Thr
                1500                1505                1510

cgt tat acg gat ata caa aca aat act tca cga gaa gag act gtc aat   5741
Arg Tyr Thr Asp Ile Gln Thr Asn Thr Ser Arg Glu Glu Thr Val Asn
            1515                1520                1525

att aaa agt gat gat tgg gga aat act cta ctt att act gag acc agt   5789
Ile Lys Ser Asp Asp Trp Gly Asn Thr Leu Leu Ile Thr Glu Thr Ser
        1530                1535                1540

ggg ata cag aaa gaa tac gtt tat tat cog gtc aat ggc gaa ggt aat   5837
Gly Ile Gln Lys Glu Tyr Val Tyr Tyr Pro Val Asn Gly Glu Gly Asn
    1545                1550                1555

agt tgc cct gcc gat ccc ttg ggt ttt tct cgg ttc tta aaa tca gtt   5885
Ser Cys Pro Ala Asp Pro Leu Gly Phe Ser Arg Phe Leu Lys Ser Val
1560                1565                1570                1575

acg caa aaa ggg tcg cct gat gct gct caa agt gtc gca aat aaa gtg   5933
Thr Gln Lys Gly Ser Pro Asp Ala Ala Gln Ser Val Ala Asn Lys Val
                1580                1585                1590

att cat tat aca tat caa aaa ttt cct act ttt acc ggc gct tat gtt   5981
Ile His Tyr Thr Tyr Gln Lys Phe Pro Thr Phe Thr Gly Ala Tyr Val
            1595                1600                1605

aag gaa tat gtc agt aaa gtc tca gag acg ata gac aat aaa ata gcg   6029
Lys Glu Tyr Val Ser Lys Val Ser Glu Thr Ile Asp Asn Lys Ile Ala
        1610                1615                1620

aga acc ttt agc tat gtt aac tca cog acg agt aaa tct cat ggt tcg   6077
Arg Thr Phe Ser Tyr Val Asn Ser Pro Thr Ser Lys Ser His Gly Ser
    1625                1630                1635

tta gca aaa ata acg tca gtg atg aat aac cag caa acg gtc acc aca   6125
Leu Ala Lys Ile Thr Ser Val Met Asn Asn Gln Gln Thr Val Thr Thr
1640                1645                1650                1655

ttt aaa tat gaa tat tca gaa agt gag atg acc aca aat gct acg gtg   6173
Phe Lys Tyr Glu Tyr Ser Glu Ser Glu Met Thr Thr Asn Ala Thr Val
                1660                1665                1670

acc ggt ttt gat ggc gca cat atg caa tcg aaa aat gtg acg tct att   6221
Thr Gly Phe Asp Gly Ala His Met Glu Ser Lys Asn Val Thr Ser Ile
            1675                1680                1685

tat acc cat cgg caa ctt cgt aaa gtt gat gta aac cac gtg att acc   6269
Tyr Thr His Arg Gln Leu Arg Lys Val Asp Val Asn His Val Ile Thr
        1690                1695                1700

gat cag tct tat gat ctt ttg ggt cgc att aca ggg caa att att gat   6317
Asp Gln Ser Tyr Asp Leu Leu Gly Arg Ile Thr Gly Gln Ile Ile Asp
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1705                1710                1715

ccc ggc acg gca aga gaa att aaa cgt aat tac gtt tat caa tat ccc   6365
Pro Gly Thr Ala Arg Glu Ile Lys Arg Asn Tyr Val Tyr Gln Tyr Pro
1720                1725                1730                1735

ggc ggt gac gaa aat gat ttt tgg ccg gtg atg ata gaa gtt gat tct   6413
Gly Gly Asp Glu Asn Asp Phe Trp Pro Val Met Ile Glu Val Asp Ser
                1740                1745                1750

caa ggc gtc aga cgt aaa acc cat tac gat ggg atg ggg cgt att tgt   6461
Gln Gly Val Arg Arg Lys Thr His Tyr Asp Gly Met Gly Arg Ile Cys
            1755                1760                1765

tcg act gaa gaa caa gat gat gat ggc gcc tgg ggc aca tcg ggg att   6509
Ser Ile Glu Glu Gln Asp Asp Asp Gly Ala Trp Gly Thr Ser Gly Ile
        1770                1775                1780

tat caa ggc aca tat cga aaa gtt ctt gcc aga caa tat gat gtt ttg   6557
Tyr Gln Gly Thr Tyr Arg Lys Val Leu Ala Arg Gln Tyr Asp Val Leu
    1785                1790                1795

ggg ccg ttg agc aag gaa att tca aat gat tgg tta tgg aat tta tct   6605
Gly Gln Leu Ser Lys Glu Ile Ser Asn Asp Trp Leu Trp Asn Leu Ser
1800                1805                1810                1815

gcc aat cct ttg gtt cgt ctt gct acc ccg ttg gtt aca acg aaa acc   6653
Ala Asn Pro Leu Val Arg Leu Ala Thr Pro Leu Val Thr Thr Lys Thr
                1820                1825                1830

tat aaa tat gat ggt tgg gga aat ctt tat agc acg gaa tac agt gat   6701
Tyr Lys Tyr Asp Gly Trp Gly Asn Leu Tyr Ser Thr Glu Tyr Ser Asp
            1835                1840                1845

ggt cgg ata gag ctg gaa atc cat gat cct att acg agg aca att act   6749
Gly Arg Ile Glu Leu Glu Ile His Asp Pro Ile Thr Arg Thr Ile Thr
        1850                1855                1860

caa ggg gtc aaa gga tta ggg atg tta aat att cag caa aat aat ttt   6797
Gln Gly Val Lys Gly Leu Gly Met Leu Asn Ile Gln Gln Asn Asn Phe
    1865                1870                1875

gag caa ccg gct tcg atc aaa gct gtg tat cct gat ggt acg ata tat   6845
Glu Gln Pro Ala Ser Ile Lys Ala Val Tyr Pro Asp Gly Thr Ile Tyr
1880                1885                1890                1895

agc acc cgt act tat cgt tat gat ggg ttt ggt cgt aca gtg acg gaa   6893
Ser Thr Arg Thr Tyr Arg Tyr Asp Gly Phe Gly Arg Thr Val Thr Glu
                1900                1905                1910

aca gat gca gaa ggt cat gct acc caa att gga tat gat gtg ttt gat   6941
Thr Asp Ala Glu Gly His Ala Thr Gln Ile Gly Tyr Asp Val Phe Asp
            1915                1920                1925

cgt ata gtg aaa aaa acg ttg cca gat gga aca ata ttt gaa tcc gct   6989
Arg Ile Val Lys Lys Thr Leu Pro Asp Gly Thr Ile Leu Glu Ser Ala
        1930                1935                1940

tat gca agt ttt agc cat gaa gaa tta att tcg gca ctg aac gtg aat   7037
Tyr Ala Ser Phe Ser His Glu Glu Leu Ile Ser Ala Leu Asn Val Asn
    1945                1950                1955

ggc aca cag ttg ggg gca tta gtt tat gat ggt ctt ggg cgg gta ata   7085
Gly Thr Gln Leu Gly Ala Leu Val Tyr Asp Gly Leu Gly Arg Val Ile
1960                1965                1970                1975
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agt gat acg gtg ggt ggt cgc aaa acg gaa tat tta tat ggg cct caa   7133
Ser Asp Thr Val Gly Gly Arg Lys Thr Glu Tyr Leu Tyr Gly Pro Gln
                1980                1985                1990

ggt gac aaa cag att cag tca att act cct tcg cat aat cag caa aat   7181
Gly Asp Lys Pro Ile Gln Ser Ile Thr Pro Ser His Asn Lys Gln Asn
            1995                2000                2005

atg gat tac ctc tac tat ctt ggt agt gtg atg tcc aaa ttt acc acg   7229
Met Asp Tyr Leu Tyr Tyr Leu Gly Ser Val Met Ser Lys Phe Thr Thr
        2010                2015                2020

ggg acc gac caa caa aac ttt cgt tat cat tcg aaa acg gga aca tta   7277
Gly Thr Asp Gln Gln Asn Phe Arg Tyr His Ser Lys Thr Gly Thr Leu
    2025                2030                2035

tta tct gcg tca gaa ggc gta tct cag act aat tac agt tat ttc cca   7325
Leu Ser Ala Ser Glu Gly Val Ser Gln Thr Asn Tyr Ser Tyr Phe Pro
2040                2045                2050                2055

tcg ggt gta tta cag cgg gaa tca ttt tta cgg gat aat aaa ccg att   7373
Ser Gly Val Leu Gln Arg Glu Ser Phe Leu Arg Asp Asn Lys Pro Ile
                2060                2065                2070

tca tcg ggc gag tac ctt tat acg atg tcc ggt ttg att caa cgt cat   7421
Ser Ser Gly Glu Tyr Leu Tyr Thr Met Ser Gly Leu Ile Gln Arg His
            2075                2080                2085

aaa gat agt ttt ggt cat aat cat gtt tat agt tac gat gct cag gga   7469
Lys Asp Ser Phe Gly His Asn His Val Tyr Ser Tyr Asp Ala Gln Gly
        2090                2095                2100

aga ttg gtc aaa acg gaa cag gat gca caa tac gct aca ttt gaa tat   7517
Arg Leu Val Lys Thr Glu Gln Asp Ala Gln Tyr Ala Thr Phe Glu Tyr
    2105                2110                2115

gac aat gtt ggg cga ttg ata acc acg acg acc aaa gac acg acg tca   7565
Asp Asn Val Gly Arg Leu Ile Thr Thr Thr Thr Lys Asp Thr Thr Ser
2120                2125                2130                2135

tta tcc caa tta gtg acg aaa atc gaa tat gat gct ttt gat cga gaa   7613
Leu Ser Gln Leu Val Thr Lys Ile Glu Tyr Asp Ala Phe Asp Arg Glu
                2140                2145                2150

ata aaa cgc tcg cta att agt gac ttc tca ata caa gtt att acc tta   7661
Ile Lys Arg Ser Leu Ile Ser Asp Phe Ser Ile Gln Val Ile Thr Leu
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agc tat acg aag aat aat caa atc agt caa cgt atc acc tcc atc gat   7709
Ser Tyr Thr Lys Asn Asn Gln Ile Ser Gln Arg Ile Thr Ser Ile Asp
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Gly Val Val Met Lys Asn Glu Arg Tyr Gln Tyr Asp Asn Asn Gln Arg
    2185                2190                2195

tta agc caa tac caa tgt gag gga gaa caa tct ccg att gat cat acg   7805
Leu Ser Gln Tyr Gln Cys Glu Gly Glu Gln Ser Pro Ile Asp His Thr
2200                2205                2210                2215

ggt cgt gta tta aat cag cag att tac cat tat gac caa tgg gga aat   7853
Gly Arg Val Leu Asn Gln Gln Ile Tyr His Tyr Asp Gln Trp Gly Asn
                2220                2225                2230
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Ile Lys Arg Leu Asp Asn Thr Tyr Arg Asp Gly Lys Glu Thr Val Asp
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tat cat ttc agt caa gcc gat cca act caa ctt att cgt att acc agc   7949
Tyr His Phe Ser Gln Ala Asp Pro Thr Gln Leu Ile Arg Ile Thr Ser
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gac aaa cag cag ata gag tta agt tat gat gct aat ggc aac cta aca   7997
Asp Lys Gln Gln Ile Glu Leu Ser Tyr Asp Ala Asn Gly Asn Leu Thr
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cgt gac gaa aaa ggg caa acg ctc att tac gat cag aat aat cgc ttg   8045
Arg Asp Glu Lys Gly Gln Thr Leu Ile Tyr Asp Gln Asn Asn Arg Leu
2280                2285                2290                2295

gta cag gtc aaa gac cgg ttg ggc aat ctg gtg tgc agc tac cag tat   8093
Val Gln Val Lys Asp Arg Leu Gly Asn Leu Val Cys Ser Tyr Gln Tyr
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gat gca ttg aac aaa tta acc gca cag gtt ttg acg aat ggt acc gtt   8141
Asp Ala Leu Asn Lys Leu Thr Ala Gln Val Leu Ala Asn Gly Thr Val
            2315                2320                2325

aat cga cag cat tat gct tcc ggt aaa gtg acg aat att caa ttg ggt   8189
Asn Arg Gln His Tyr Ala Ser Gly Lys Val Thr Asn Ile Gln Leu Gly
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gat gaa gcg att act tgg ttg agc agt gat aag caa cga att gga cat   8237
Asp Glu Ala Ile Thr Trp Leu Ser Ser Asp Lys Gln Arg Ile Gly His
    2345                2350                2355

caa agt gcc aag aat ggt caa tca gtc tac tat caa tat ggt att gac   8285
Gln Ser Ala Lys Asn Gly Gln Ser Val Tyr Tyr Gln Tyr Gly Ile Asp
2360                2365                2370                2375

cat aac agt acg gtt atc gcc agt cag aac gaa aac gag ttg atg gct   8333
His Asn Ser Thr Val Ile Ala Ser Gln Asn Glu Asn Glu Leu Met Ala
                2380                2385                2390

tta tcc tat aca cct tat ggc ttt agg agt tta att tcc tca tta ccg   8381
Leu Ser Tyr Thr Pro Tyr Gly Phe Arg Ser Leu Ile Ser Ser Leu Pro
            2395                2400                2405

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Gly Leu Asn Gly Ala Gln Val Asp Pro Val Thr Gly Trp Tyr Phe Leu
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ggt aac gga tat cgt gtt ttc aac ccg gtt ctc atg agg ttt cac agc   8477
Gly Asn Gly Tyr Arg Val Phe Asn Pro Val Leu Met Arg Phe His Ser
    2425                2430                2435

ccc gat agt tgg agt cct ttt ggt cgg gga ggg att aac cct tat acc   8525
Pro Asp Ser Trp Ser Pro Phe Gly Arg Gly Gly Ile Asn Pro Tyr Thr
2440                2445                2450                2455

tat tgc caa ggc gat ccc ata aac cgg att gat ctg aac ggt cat ctt   8573
Tyr Cys Gln Gly Asp Pro Ile Asn Arg Ile Asp Leu Asn Gly His Leu
                2460                2465                2470

agt gcc ggc ggg ata tta ggc att gtg cta ggg gca att ggc atc att   8621
Ser Ala Gly Gly Ile Leu Gly Ile Val Leu Gly Ala Ile Gly Ile Ile
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Val Gly Ile Val Ser Leu Gly Ala Gly Ala Ala Ile Ser Ala Ala Gly Leu
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Ile Ala Ala Gly Gly Ala Leu Gly Ala Ile Ala Ser Thr Ser Ala Leu
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Ala Val Thr Ala Thr Val Ile Gly Leu Ala Ala Asp Ser Ile Gly Ile
2520                2525                2530                2535

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Ala Ser Ala Ala Leu Ser Glu Lys Asp Pro Lys Thr Ser Gly Ile Leu
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Asn Trp Ile Ser Ala Gly Leu Gly Val Leu Ser Phe Gly Ile Ser Ala
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Ile Thr Phe Thr Ser Ser Leu Val Lys Ser Ala Arg Ser Gly Ser Gln
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Ala Val Ser Ala Gly Val Ile Gly Ser Val Pro Leu Glu Phe Gly Glu
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Val Ala Ser Arg Ser Ser Arg Arg Trp Asp Ile Ala Leu Ser Ser Ile
2600                2605                2610                2615

tcg ttg ggc gca aat gcg gcg tct ctc tct acg ggg ata gcg gcg gcg   9053
Ser Leu Gly Ala Asn Ala Ala Ser Leu Ser Thr Gly Ile Ala Ala Ala
                2620                2625                2630

gcg gtt gca gac agt aat gcg aat gca gct aat att ctg gga tgg gta   9101
Ala Val Ala Asp Ser Asn Ala Asn Ala Ala Asn Ile Leu Gly Trp Val
            2635                2640                2645

tcc ttt ggt ttt ggt gca gta tcg aca acc tca gga ata atc gag ctt   9149
Ser Phe Gly Phe Gly Ala Val Ser Thr Thr Ser Gly Ile Ile Glu Leu
        2650                2655                2660

acg cgt aca gct tat gca gtg aat cat cag act tgg gaa ctg agt tca   9197
Thr Arg Thr Ala Tyr Ala Val Asn His Gln Thr Trp Glu Leu Ser Ser
    2665                2670                2675

tca gca ggt act tcg gag gaa gtg aag cct ata cgt tgt ctc gtt tca   9245
Ser Ala Gly Thr Ser Glu Glu Val Lys Pro Ile Arg Cys Leu Val Ser
2680                2685                2690                2695

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His Arg Trp Asn Gln Lys Gln
                2700

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Met Gln Arg Ala Gln Arg Val Val Ile Thr Gly Met Gly Ala Val Thr
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Pro Ile Gly Glu Asp Val Glu Ser Cys Trp Gln Ser Ile Ile Glu Lys
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Gln His Arg Phe His Arg Ile Glu Phe Pro Asp Ser Phe Ile Asn Ser
         35                  40                  45

Arg Phe Phe Ser Phe Leu Ala Pro Asn Pro Ser Arg Tyr Gln Leu Leu
     50                  55                  60

Pro Lys Lys Leu Thr His Thr Leu Ser Asp Cys Gly Lys Ala Ala Leu
 65                  70                  75                  80

Lys Ala Thr Tyr Gln Ala Phe Thr Gln Ala Phe Gly Val Asn Ile Ser
                 85                  90                  95

Pro Val Glu Tyr Tyr Asp Lys Tyr Glu Cys Gly Val Ile Leu Gly Ser
            100                 105                 110

Gly Trp Gly Ala Ile Asp Asn Ala Gly Asp His Ala Cys Gln Tyr Lys
        115                 120                 125

Gln Ala Lys Leu Ala His Pro Met Ser Asn Leu Ile Thr Met Pro Ser
    130                 135                 140

Ser Met Thr Ala Ala Cys Ser Ile Met Tyr Gly Leu Arg Gly Tyr Gln
145                 150                 155                 160

Asn Thr Val Met Ala Ala Cys Ala Thr Gly Thr Met Ala Ile Gly Asp
                165                 170                 175

Ala Phe Glu Ile Ile Arg Ser Gly Arg Ala Lys Cys Met Ile Ala Gly
            180                 185                 190

Ala Ala Glu Ser Leu Thr Arg Glu Cys Asn Ile Trp Ser Ile Asp Val
        195                 200                 205

Leu Asn Ala Leu Ser Lys Glu Gln Ala Asp Pro Asn Leu Ala Cys Cys
    210                 215                 220

Pro Phe Ser Leu Asp Arg Ser Gly Phe Val Leu Ala Glu Gly Ala Ala
225                 230                 235                 240

Val Val Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr
                245                 250                 255

Ile Leu Ala Glu Ile Lys Gly Tyr Ala Gln Tyr Ser Asp Ala Val Asn
            260                 265                 270

Leu Thr Arg Pro Thr Glu Asp Ile Glu Pro Lys Ile Leu Ala Ile Thr
        275                 280                 285
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Lys Ala Ile Glu Gln Ala Gln Ile Ser Pro Lys Asp Ile Asp Tyr Ile
290 295 300

Asn Ala His Gly Thr Ser Thr Pro Leu Asn Asp Leu Tyr Glu Thr Gln
305 310 315 320

Ala Ile Lys Ala Ala Leu Gly Gln Tyr Ala Tyr Gln Val Pro Ile Ser
325 330 335

Ser Thr Lys Ser Tyr Thr Gly His Leu Ile Ala Ala Ala Gly Ser Phe
340 345 350

Glu Thr Ile Val Cys Val Lys Ala Leu Ala Glu Asn Cys Leu Pro Ala
355 360 365

Thr Leu Asn Leu His Arg Ala Asp Pro Asp Cys Asp Leu Asn Tyr Leu
370 375 380

Pro Asn Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile
385 390 395 400

Ser Ala Gly Phe Gly Gly His Asn Ala Ala Leu Val Ile Ala Lys Val
405 410 415

Arg

<210> 3
<211> 253
<212> PRT
<213> Photorhabdus luminescens

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Met Glu Asp Ile Glu His Trp Ser Asn Phe Ser Gly Asp Phe Asn Pro
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Ile His Tyr Ser Ala Lys Ser Glu Ser Leu Arg Asn Ile Gln Gln His
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Pro Val Gln Gly Met Leu Ser Leu Leu Tyr Val Arg Gln Gln Phe Ser
35 40 45

Gln Leu Thr Ser Ala Phe Thr Thr Gly Ile Leu Asn Ile Asp Ala Ser
50 55 60

Phe Arg Gln Tyr Val Tyr Thr Ala Leu Pro His Gln Leu Arg Ile Asn
65 70 75 80

Thr Lys Asn Lys Thr Phe Lys Leu Glu Asn Pro Ser Lys Glu Asn Thr
85 90 95

Leu Phe Gly Asn Thr Ser Val Glu Asn Thr Met Glu Ser Ile Glu Asp
100 105 110

Trp Ile Val Gln Asp Asn Cys Gln Lys Leu Thr Ile Thr Gly Glu Glu
115 120 125

Val Cys Glu Lys Tyr Ala Val Phe Arg Tyr Tyr Phe Pro Ser Val Thr
130 135 140

Ser Ile Gly Trp Phe Leu Asp Ala Leu Ala Phe His Leu Ile Ile Asn
145 150 155 160

Ser Thr Gly Phe Leu Asn Phe Glu His Tyr His Phe Asn Gln Leu Gln
165 170 175

Asp Tyr Leu Ser Gln Ser Phe Thr Leu His Thr Gly Gln Ala Ile Lys
180 185 190

Ile Arg Lys Glu Ile Val Asn Ser Thr Val Leu Leu Ser Ser Pro Asp
195 200 205

Ile Cys Val Glu Leu Asn Pro Pro Leu Leu Ile Lys Asn Gly Asp Lys
210 215 220

Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu Tyr Asp Lys Lys Pro
225 230 235 240

Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys Met Lys
245 250

<210> 4
<211> 186
<212> PRT
<213> Photorhabdus luminescens

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Met Asn Val Leu Glu Gln Gly Lys Val Ala Ala Leu Tyr Ser Ala Tyr
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Ser Glu Thr Glu Gly Ser Ser Trp Val Gly Asn Leu Cys Cys Phe Ser
20 25 30

Ser Asp Arg Glu His Leu Pro Ile Ile Val Asn Gly Arg Arg Phe Leu
35 40 45

Ile Glu Phe Val Ile Pro Asp His Leu Leu Asp Lys Thr Val Lys Pro
50 55 60

Arg Val Phe Asp Leu Asp Ile Asn Lys Gln Pro Leu Leu Arg Arg Asp
65 70 75 80

His Arg Glu Ile Asn Ile Tyr Leu Leu Gly Glu Gly Asn Phe Met Asp
85 90 95

Arg Thr Thr Thr Asp Lys Asn Leu Phe Glu Leu Asn Glu Asp Gly Ser
100 105 110

Leu Phe Ile Lys Thr Leu Arg His Ala Leu Gly Lys Tyr Val Ala Ile
115 120 125

Asn Pro Ser Thr Thr Gln Phe Ile Phe Phe Ala Gln Gly Lys Tyr Ser
130 135 140

Glu Phe Ile Met Asn Ala Leu Lys Thr Val Glu Asp Glu Leu Ser Lys
145 150 155 160

Arg Tyr Arg Val Arg Ile Ile Pro Glu Leu Gln Gly Pro Tyr Tyr Gly
165 170 175

Phe Glu Leu Asp Ile Leu Ser Ile Thr Ala
180 185

<210> 5
<211> 258
<212> PRT
<213> Photorhabdus luminescens

<400> 5

Met Glu Lys Lys Ile Thr Thr Phe Thr Ile Glu Lys Thr Asp
1 5 10

Asp Asn Phe Tyr Ala Asn Gly Arg His Gln Cys Met Val Lys Ile Ser
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Val Leu Lys Gln Glu Tyr Arg Asn Gly Asp Trp Ile Lys Leu Ala Leu
35 40 45

Ser Glu Ala Glu Lys Arg Ser Ile Gln Val Ala Ala Leu Ser Asp Ser
50 55 60

Leu Ile Tyr Asp Gln Leu Lys Met Pro Ser Gly Trp Thr Thr Thr Asp
65 70 75

Ala Arg Asn Lys Phe Asp Leu Gly Leu Leu Asn Gly Val Tyr His Ala
80 85 90

Asp Ala Phe Ile Asp Glu Gln Val Thr Asp Arg Ala Gly Asp Cys Cys
95 100 105 110

Thr Asn Glu Asn Tyr Gln Asn Ser Val Lys Ser Val Pro Glu Ile Ile
115 120 125

Tyr Arg Tyr Val Ser Ser Asn Arg Thr Ser Thr Glu Tyr Leu Met Ala
130 135 140

Lys Met Thr Phe Glu Asp Thr Asp Gly Lys Arg Thr Leu Thr Thr Asn
145 150 155

Met Ser Val Gly Asp Glu Val Phe Asp Ser Lys Val Leu Leu Lys Ala
160 165 170

Ile Ala Pro Tyr Ala Ile Asn Thr Asn Gln Leu His Glu Asn Ile Asn
175 180 185 190

Thr Leu Phe Asp Lys Thr Glu Glu Pro Thr Lys Ser Asp Thr His Ile
195 200 205

Gln Ile Ile Asn Leu Tyr Arg Trp Thr Leu Pro Tyr His Leu Arg Ile
210 215 220

Leu Glu Gly Asn Asp Ser Thr Val Asn Arg Ile Tyr Val Leu Gly Lys
225 230 235

Glu Pro Ser Asn Asp Arg Phe Leu Thr Arg Gly Arg Val Phe Lys Arg
240 245 250

Gly Thr His Met
255

<210> 6
<211> 1584
<212> PRT
<213> Photorhabdus luminescens

<400> 6

Met Lys Ala Thr Asp Ile Tyr Ser Asn Ala Pro Asn Phe Gly Ser Tyr
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Ile Asn Thr Gly Val Asp Pro Arg Thr Gly Gln Tyr Ser Ala Asn Ile
20 25 30

Asn Ile Ile Thr Leu Arg Pro Asn Asn Val Gly Asn Ser Glu Gln Thr
35 40 45

Leu Ser Leu Ser Phe Ser Pro Leu Thr Thr Leu Asn Asn Gly Phe Gly
50 55 60

Ile Gly Trp Arg Phe Ser Leu Thr Thr Leu Asp Ile Lys Thr Leu Thr
65 70 75 80

Phe Ser Arg Ala Asn Gly Glu Gln Phe Lys Cys Lys Pro Leu Pro Pro
85 90 95

Asn Asn Asn Asp Leu Ser Phe Lys Asp Lys Lys Leu Lys Asp Leu Arg
100 105 110

Val Tyr Lys Leu Asp Ser Asn Thr Phe Tyr Val Tyr Asn Lys Asn Gly
115 120 125

Ile Ile Glu Ile Leu Lys Arg Ile Gly Ser Ser Asp Ile Ala Lys Thr
130 135 140

Val Ala Leu Glu Phe Pro Asp Gly Glu Ala Phe Asp Leu Ile Tyr Asn
145 150 155 160

Ser Arg Phe Ala Leu Ser Glu Ile Lys Tyr Arg Val Thr Gly Lys Thr
165 170 175

Tyr Leu Lys Leu Asn Tyr Ser Gly Asn Asn Cys Thr Ser Val Glu Tyr
180 185 190

Pro Asp Asp Asn Asn Ile Ser Ala Lys Ile Ala Phe Asp Tyr Arg Asn
195 200 205

Asp Tyr Leu Ile Thr Val Thr Val Pro Tyr Asp Ala Ser Gly Pro Ile
210 215 220

Asp Ser Ala Arg Phe Lys Met Thr Tyr Gln Thr Leu Lys Gly Val Phe
225 230 235 240

Pro Val Ile Ser Thr Phe Arg Thr Pro Thr Gly Tyr Val Glu Leu Val
245 250 255

Ser Tyr Lys Glu Asn Gly His Lys Val Thr Asp Thr Glu Tyr Ile Pro
260 265 270

Tyr Ala Ala Ala Leu Thr Ile Gln Pro Gly Asn Gly Gln Pro Ala Val
275 280 285

Ser Lys Ser Tyr Glu Tyr Ser Ser Val His Asn Phe Leu Gly Tyr Ser
290 295 300

Ser Gly Arg Thr Ser Phe Asp Ser Ser Gln Asp Asn Leu Tyr Leu Val
305 310 315 320

Thr Gly Lys Tyr Thr Tyr Ser Ser Ile Glu Arg Val Leu Asp Gly Gln
325 330 335

Ser Val Val Ser Val Ile Glu Arg Val Phe Asn Lys Phe His Leu Met
340 345 350

Thr Lys Glu Ala Lys Thr Gln Asp Asn Lys Arg Ile Thr Thr Glu Ile
355 360 365

Thr Tyr Asn Glu Asp Leu Ser Lys Ser Phe Ser Glu Gln Pro Glu Asn
370 375 380

Leu Gln Gln Pro Ser Arg Val Leu Thr Arg Tyr Thr Asp Ile Gln Thr
385 390 395 400

Asn Thr Ser Arg Glu Glu Thr Val Asn Ile Lys Ser Asp Asp Trp Gly
405 410 415

Asn Thr Leu Leu Ile Thr Glu Thr Ser Gly Ile Gln Lys Glu Tyr Val
420 425 430

Tyr Tyr Pro Val Asn Gly Glu Gly Asn Ser Cys Pro Ala Asp Pro Leu
435 440 445

Gly Phe Ser Arg Phe Leu Lys Ser Val Thr Gln Lys Gly Ser Pro Asp
450 455 460

Ala Ala Gln Ser Val Ala Asn Lys Val Ile His Tyr Thr Tyr Gln Lys
465 470 475 480

Phe Pro Thr Phe Thr Gly Ala Tyr Val Lys Glu Tyr Val Ser Lys Val
485 490 495

Ser Glu Thr Ile Asp Asn Lys Ile Ala Arg Thr Phe Ser Tyr Val Asn
500 505 510

Ser Pro Thr Ser Lys Ser His Gly Ser Leu Ala Lys Ile Thr Ser Val
515 520 525

Met Asn Asn Gln Gln Thr Val Thr Thr Pro Lys Tyr Glu Tyr Ser Glu
530 535 540

Ser Glu Met Thr Thr Asn Ala Thr Val Thr Gly Phe Asp Gly Ala His
545 550 555 560

Met Glu Ser Lys Asn Val Thr Ser Ile Tyr Thr His Arg Gln Leu Arg
565 570 575

Lys Val Asp Val Asn His Val Ile Thr Asp Gln Ser Tyr Asp Leu Leu
580 585 590

Gly Arg Ile Thr Gly Gln Ile Ile Asp Pro Gly Thr Ala Arg Glu Ile
595 600 605

Lys Arg Asn Tyr Val Tyr Gln Tyr Pro Gly Gly Asp Glu Asn Asp Phe
610 615 620

Trp Pro Val Met Ile Glu Val Asp Ser Gln Gly Val Arg Arg Lys Thr
625 630 635 640

His Tyr Asp Gly Met Gly Arg Ile Cys Ser Ile Glu Glu Gln Asp Asp
645 650 655

Asp Gly Ala Trp Gly Thr Ser Gly Ile Tyr Gln Gly Thr Tyr Arg Lys
660 665 670

Val Leu Ala Arg Gln Tyr Asp Val Leu Gly Gln Leu Ser Lys Glu Ile
675 680 685

Ser Asn Asp Trp Leu Trp Asn Leu Ser Ala Asn Pro Leu Val Arg Leu
690 695 700

Ala Thr Pro Leu Val Thr Thr Lys Thr Tyr Lys Tyr Asp Gly Trp Gly
705 710 715 720

Asn Leu Tyr Ser Thr Glu Tyr Ser Asp Gly Arg Ile Glu Leu Glu Ile

725 730 735

His Asp Pro Ile Thr Arg Thr Ile Thr Gln Gly Val Lys Gly Leu Gly
740 745 750

Met Leu Asn Ile Gln Gln Asn Asn Phe Glu Glu Pro Ala Ser Ile Lys
755 760 765

Ala Val Tyr Pro Asp Gly Thr Ile Tyr Ser Thr Arg Thr Tyr Arg Tyr
770 775 780

Asp Gly Phe Gly Arg Thr Val Thr Glu Thr Asp Ala Glu Gly His Ala
785 790 795 800

Thr Gln Ile Gly Tyr Asp Val Phe Asp Arg Ile Val Lys Lys Thr Leu
805 810 815

Pro Asp Gly Thr Ile Leu Glu Ser Ala Tyr Ala Ser Phe Ser His Glu
820 825 830

Glu Leu Ile Ser Ala Leu Asn Val Asn Gly Thr Gln Leu Gly Ala Leu
835 840 845

Val Tyr Asp Gly Leu Gly Arg Val Ile Ser Asp Thr Val Gly Gly Arg
850 855 860

Lys Thr Glu Tyr Leu Tyr Gly Pro Gln Gly Asp Lys Pro Ile Glu Ser
865 870 875 880

Ile Thr Pro Ser His Asn Lys Gln Asn Met Asp Tyr Leu Tyr Tyr Leu
885 890 895

Gly Ser Val Met Ser Lys Phe Thr Thr Gly Thr Asp Gln Gln Asn Phe
900 905 910

Arg Tyr His Ser Lys Thr Gly Thr Leu Leu Ser Ala Ser Glu Gly Val
915 920 925

Ser Gln Thr Asn Tyr Ser Tyr Pro Pro Ser Gly Val Leu Gln Arg Glu
930 935 940

Ser Phe Leu Arg Asp Asn Lys Pro Ile Ser Ser Gly Glu Tyr Leu Tyr
945 950 955 960

Thr Met Ser Gly Leu Ile Gln Arg His Lys Asp Ser Phe Gly His Asn
965 970 975

His Val Tyr Ser Tyr Asp Ala Gln Gly Arg Leu Val Lys Thr Glu Gln
980 985 990

Asp Ala Gln Tyr Ala Thr Phe Glu Tyr Asp Asn Val Gly Arg Leu Ile
995 1000 1005

Thr Thr Thr Thr Lys Asp Thr Thr Ser Leu Ser Gln Leu Val Thr Lys
1010 1015 1020

Ile Glu Tyr Asp Ala Phe Asp Arg Glu Ile Lys Arg Ser Leu Ile Ser
025 1030 1035 1040

Asp Phe Ser Ile Gln Val Ile Thr Leu Ser Tyr Thr Lys Asn Asn Gln
1045 1050 1055

Ile Ser Gln Arg Ile Thr Ser Ile Asp Gly Val Val Met Lys Asn Glu
1060 1065 1070

Arg Tyr Gln Tyr Asp Asn Asn Gln Arg Leu Ser Gln Tyr Gln Cys Glu
1075 1080 1085

Gly Glu Gln Ser Pro Ile Asp His Thr Gly Arg Val Leu Asn Gln Gln
1090 1095 1100

Ile Tyr His Tyr Asp Gln Trp Gly Asn Ile Lys Arg Leu Asp Asn Thr
105 1110 1115 1120

Tyr Arg Asp Gly Lys Glu Thr Val Asp Tyr His Phe Ser Gln Ala Asp
1125 1130 1135

Pro Thr Gln Leu Ile Arg Ile Thr Ser Asp Lys Gln Gln Ile Glu Leu
1140 1145 1150

Ser Tyr Asp Ala Asn Gly Asn Leu Thr Arg Asp Glu Lys Gly Gln Thr
1155 1160 1165

Leu Ile Tyr Asp Gln Asn Asn Arg Leu Val Gln Val Lys Asp Arg Leu
1170 1175 1180

Gly Asn Leu Val Cys Ser Tyr Gln Tyr Asp Ala Leu Asn Lys Leu Thr
185 1190 1195 1200

Ala Gln Val Leu Ala Asn Gly Thr Val Asn Arg Gln His Tyr Ala Ser
1205 1210 1215

Gly Lys Val Thr Asn Ile Gln Leu Gly Asp Glu Ala Ile Thr Trp Leu
1220 1225 1230

Ser Ser Asp Lys Gln Arg Ile Gly His Gln Ser Ala Lys Asn Gly Gln
1235 1240 1245

Ser Val Tyr Tyr Gln Tyr Gly Ile Asp His Asn Ser Thr Val Ile Ala
1250 1255 1260

Ser Gln Asn Glu Asn Glu Leu Met Ala Leu Ser Tyr Thr Pro Tyr Gly
265 1270 1275 1280

Phe Arg Ser Leu Ile Ser Ser Leu Pro Gly Leu Asn Gly Ala Gln Val
1285 1290 1295

Asp Pro Val Thr Gly Trp Tyr Phe Leu Gly Asn Gly Tyr Arg Val Phe
1300 1305 1310

Asn Pro Val Leu Met Arg Phe His Ser Pro Asp Ser Trp Ser Pro Phe
1315 1320 1325

Gly Arg Gly Gly Ile Asn Pro Tyr Thr Tyr Cys Gln Gly Asp Pro Ile
1330 1335 1340

Asn Arg Ile Asp Leu Asn Gly His Leu Ser Ala Gly Gly Ile Leu Gly
345 1350 1355 1360

Ile Val Leu Gly Ala Ile Gly Ile Ile Val Gly Ile Val Ser Leu Gly
1365 1370 1375

Ala Gly Ala Ala Ile Ser Ala Gly Leu Ile Ala Ala Gly Gly Ala Leu
1380 1385 1390

Gly Ala Ile Ala Ser Thr Ser Ala Leu Ala Val Thr Ala Thr Val Ile
1395 1400 1405

Gly Leu Ala Ala Asp Ser Ile Gly Ile Ala Ser Ala Ala Leu Ser Glu
1410 1415 1420

Lys Asp Pro Lys Thr Ser Gly Ile Leu Asn Trp Ile Ser Ala Gly Leu
425 1430 1435 1440

Gly Val Leu Ser Phe Gly Ile Ser Ala Ile Thr Phe Thr Ser Ser Leu
1445 1450 1455

Val Lys Ser Ala Arg Ser Gly Ser Gln Ala Val Ser Ala Gly Val Ile
1460 1465 1470

Gly Ser Val Pro Leu Glu Phe Gly Glu Val Ala Ser Arg Ser Ser Arg
1475 1480 1485

Arg Trp Asp Ile Ala Leu Ser Ser Ile Ser Leu Gly Ala Asn Ala Ala
1490 1495 1500

Ser Leu Ser Thr Gly Ile Ala Ala Ala Ala Val Ala Asp Ser Asn Ala
505 1510 1515 1520

Asn Ala Ala Asn Ile Leu Gly Trp Val Ser Phe Gly Phe Gly Ala Val
1525 1530 1535

Ser Thr Thr Ser Gly Ile Ile Glu Leu Thr Arg Thr Ala Tyr Ala Val
1540 1545 1550

Asn His Gln Thr Trp Glu Leu Ser Ser Ser Ala Gly Thr Ser Glu Glu
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Val Lys Pro Ile Arg Cys Leu Val Ser His Arg Trp Asn Gln Lys Gln
1570 1575 1580

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<223> Description of Artificial Sequence:oligonucleotide

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<223> Description of Artificial Sequence:oligonucleotide

<400> 8
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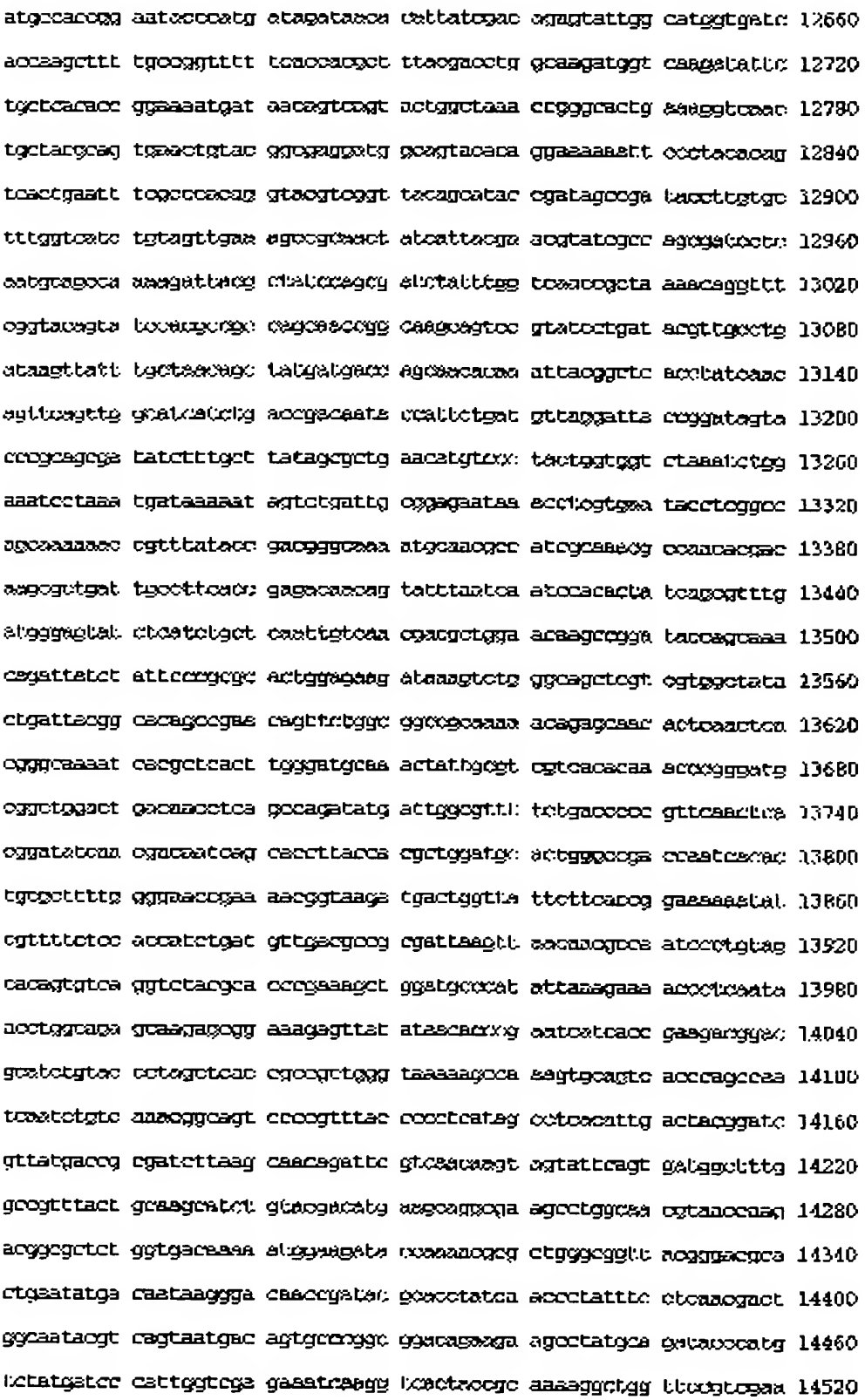

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Ala Asn Gly Asp Thr Asp Ile Arg Ile Thr Arg His Gln Tyr Asp Ser
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Leu Gly His Leu Ser Gln Ser Thr Asp Pro Arg Leu Tyr Glu Ala Lys
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Gln Lys Ser Asn Phe Leu Trp Gln Tyr Asp Leu Thr Gly Asn Ile Leu
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Cys Thr Glu Ser Val Asp Ala Gly Arg Thr Val Thr Leu Asn Asp Ile
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Arg Gln Tyr Glu Thr Ser Ser Leu Pro Gly Arg Leu Leu Ser Val Thr
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gct ggc aat agc gaa gca gag aaa aac cat aat ctt gcc agc cag tgc 15656
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Val Arg His Tyr Asp Thr Ala Gly Val Thr Arg Leu Glu Ser Leu Ser
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Leu Thr Gly Thr Val Leu Ser Gln Ser Ser Gln Leu Leu Ser Asp Thr
    180                 185                 190

caa gaa gct agc tgg aca ggt gat aat gaa acc gtc tgg caa aac atg   15800
Gln Glu Ala Ser Trp Thr Gly Asp Asn Glu Thr Val Trp Gln Asn Met
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Leu Ala Asp Asp Ile Tyr Thr Thr Leu Ser Ala Phe Asp Ala Thr Gly
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Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly Asn Ile Gln Arg Leu Thr
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Tyr Asp Val Ala Gly Gln Leu Asn Gly Ser Trp Leu Thr Leu Lys Asp
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Gln Pro Glu Gln Val Ile Ile Arg Ser Leu Thr Tyr Ser Ala Ala Gly
    260                 265                 270

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Gln Lys Leu Arg Glu Glu His Gly Asn Gly Val Ile Thr Glu Tyr Ser
275                 280                 285                 290

tat gaa ccg gaa acc caa cag ctt atc ggt acc aaa acc cac cgt ccg   16088
Tyr Glu Pro Glu Thr Gln Gln Leu Ile Gly Thr Lys Thr His Arg Pro
                295                 300                 305

tca gat gcc aaa gtg ttg caa gat cta cgt tat gag tat gac ccg gta   16136
Ser Asp Ala Lys Val Leu Gln Asp Leu Arg Tyr Glu Tyr Asp Pro Val
            310                 315                 320

ggc aat gtc atc agt atc cgt aat gac gca gaa gcc acc cgc ttc tgg   16184
Gly Asn Val Ile Ser Ile Arg Asn Asp Ala Glu Ala Thr Arg Phe Trp
        325                 330                 335

cac aat cag aaa gtg gcg ccg gaa aac act tat acc tac gac tcc ttg   16232
His Asn Gln Lys Val Ala Pro Glu Asn Thr Tyr Thr Tyr Asp Ser Leu
    340                 345                 350

tat cag ctt atc agc gca acc ggg cgt gag atg gcg aat ata ggt cag   16280
Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu Met Ala Asn Ile Gly Gln
355                 360                 365                 370

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Gln Ser Asn Gln Leu Pro Ser Leu Thr Leu Pro Ser Asp Asn Asn Thr
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Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr Asp Arg Gly Gly Asn Leu
            390                 395                 400

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Thr Lys Ile Gln His Ser Ser Pro Ala Thr Gln Asn Asn Tyr Thr Thr
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Thr Glu Asp Pro Ala Gln Val Asp Ala Leu Phe Asp Ala Gly Gly His
435                 440                 445                 450

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Gln Asn Thr Leu Ile Ser Gly Gln Asn Leu Asn Trp Asn Thr Arg Gly
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gaa cta caa cat gtg acg ttg gtg aaa cgg gac aag ggc gcc aat gat  16616
Glu Leu Gln His Val Thr Leu Val Lys Arg Asp Lys Gly Ala Asn Asp
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Asp Arg Glu Trp Tyr Arg Tyr Ser Ser Asp Gly Arg Arg Ile Leu Lys
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Ile Asn Glu Gln Gln Thr Ser Ser Asn Ser Gln Thr Gln Arg Ile Thr
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Tyr Leu Pro Ser Leu Glu Leu Arg Leu Thr Gln Asn Ser Thr Ile Thr
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Thr Glu Asp Leu Gln Val Ile Thr Val Gly Glu Ala Gly Arg Ala Gln
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Val Arg Val Leu His Trp Asp Ser Gly Gln Pro Glu Asp Ile Asp Asn
            550                 555                 560

aat cag cta cgt tat agc tac gat aat ctt atc ggt tcc agt caa ctt  16904
Asn Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser Gln Leu
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Glu Leu Asp Ser Lys Gly Glu Ile Ile Ser Glu Glu Glu Tyr Tyr Pro
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Val Arg Asn Asn Pro Val Thr Leu Leu Asp Pro Asp Gly Leu Met Pro
    660                 665                 670

aca att gca gaa cgc ata gca gca ctg caa aaa aat aaa gta gca gat  17240
Thr Ile Ala Glu Arg Ile Ala Ala Leu Gln Lys Asn Lys Val Ala Asp
675                 680                 685                 690
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tca gcg cct tcg cca aca aat gcc aca aac gta ggg ata aac atc cgc   17280
Ser Ala Pro Ser Pro Thr Asn Ala Thr Asn Val Ala Ile Asn Ile Arg
                695                 700                 705

ccg ccc gta gca cca aaa cct acc tta ccc aaa gca tca acg agt agc   17328
Pro Pro Val Ala Pro Lys Pro Thr Leu Pro Lys Ala Ser Thr Ser Ser
            710                 715                 720

caa tca act aca tac ccc atc aaa tct gca agc ata aaa ccg acg acg   17376
Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro Thr Thr
        725                 730                 735

tcg ggg tca tcc atc acc gct cca ctg agt cca gta gga aat aaa tct   17424
Ser Gly Ser Ser Ile Thr Ala Pro Leu Ser Pro Val Gly Asn Lys Ser
    740                 745                 750

act cct gaa ata tct ctt cca gaa agc act caa agc aat tct tca agc   17472
Thr Pro Glu Ile Ser Leu Pro Glu Ser Thr Gln Ser Asn Ser Ser Ser
755                 760                 765                 770

gct att tca aca aat cta cag aaa aag tca ttt act tta tat aga gcg   17520
Ala Ile Ser Thr Asn Leu Gln Lys Lys Ser Phe Thr Leu Tyr Arg Ala
                775                 780                 785

gat aat aga tcc ttt gaa gac atg cag agt aaa ttc cct gaa gga ttt   17568
Asp Asn Arg Ser Phe Glu Asp Met Gln Ser Lys Phe Pro Glu Gly Phe
            790                 795                 800

aaa gcc tgg act cct cta gat act aag atg gca agg cag ttt gct agt   17616
Lys Ala Trp Thr Pro Leu Asp Thr Lys Met Ala Arg Gln Phe Ala Ser
        805                 810                 815

gtc ttt att ggt cag aaa gat acc tct aat tta cct aaa gaa aca gtc   17664
Val Phe Ile Gly Gln Lys Asp Thr Ser Asn Leu Pro Lys Glu Thr Val
    820                 825                 830

aag aat ata aac aca tgg gga acc aaa cca aaa tta aat gat ctc tca   17712
Lys Asn Ile Asn Thr Trp Gly Thr Lys Pro Lys Leu Asn Asp Leu Ser
835                 840                 845                 850

act tac ata aaa tat acc agg gac aaa tct aca gta tgg gtc tct act   17760
Thr Tyr Ile Lys Tyr Thr Lys Asp Lys Ser Thr Val Trp Val Ser Thr
                855                 860                 865

gca att aat act gaa gca ggt ggg caa agt tca ggg gct cca ctc cat   17808
Ala Ile Asn Thr Glu Ala Gly Gly Gln Ser Ser Gly Ala Pro Leu His
            870                 875                 880

gaa atc aat atg gat ctt tat gag ttt acc atc gac ggg caa aag cta   17856
Glu Ile Asn Met Asp Leu Tyr Glu Phe Thr Ile Asp Gly Gln Lys Leu
        885                 890                 895

aat cca cta cca agg gga aga tct aaa gac agg gtg cct tca cta tta   17904
Asn Pro Leu Pro Arg Gly Arg Ser Lys Asp Arg Val Pro Ser Leu Leu
    900                 905                 910

ctt gac aca cca gaa ata gaa aca gca tcc ata att gca ctt aat cat   17952
Leu Asp Thr Pro Glu Ile Glu Thr Ala Ser Ile Ile Ala Leu Asn His
915                 920                 925                 930

gga cag gta aat gat gca gaa gtt tca ttc cta aca aca att ccg ctt   18000
Gly Pro Val Asn Asp Ala Glu Val Ser Phe Leu Thr Thr Ile Pro Leu
                935                 940                 945
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aaa aat gta aaa cct tat aag aga taa cgaaaaatta atattcttta 18055
Lys Asn Val Lys Pro Tyr Lys Arg
950 955

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tcaatttact tt atg att tta aaa gga ata aat atg aat tcg cct gta aaa 23806

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                Met Ile Leu Lys Gly Il  Asn Met Asn Ser Pro Val Lys
                                960                 965

gag ata cct gat gta tta aaa atc cag tgt ggt ttt cag tgt ctg aca  23854
Glu Ile Pro Asp Val Leu Lys Ile Gln Cys Gly Phe Gln Cys Leu Thr
    970                 975                 980

gac att agc cac agc tct ttt aac gaa ttt cac cag caa gta tcc gaa  23902
Asp Ile Ser His Ser Ser Phe Asn Glu Phe His Gln Gln Val Ser Glu
985                 990                 995                1000

cac ctc tcc tgg tcc gaa gca cac gac tta tat cat gat gca caa cag  23950
His Leu Ser Trp Ser Glu Ala His Asp Leu Tyr His Asp Ala Gln Gln
                1005                1010                1015

gcc caa aag gat aat cgg ctg tat gaa gcg cgt atc ctt aaa cgc acg  23998
Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala Arg Ile Leu Lys Arg Thr
            1020                1025                1030

aat cct caa tta caa aat gct gta cat ctt gcc atc gta gcg cct aat  24046
Asn Pro Gln Leu Gln Asn Ala Val His Leu Ala Ile Val Ala Pro Asn
        1035                1040                1045

gct gaa ctg ata ggc tat aac aac caa ttt agc ggc agg gcc agt caa  24094
Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln
    1050                1055                1060

tat gtc gcg ccg ggt acc gtt tcc tcc atg ttc tcc ccc gcc gct tat  24142
Tyr Val Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr
1065                1070                1075                1080

ttg act gag ctt tat cgt gaa gca cgc aat tta cac gcc agc gat tcc  24190
Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser
                1085                1090                1095

gtt tat cgc ctg gat act cgc cgc cca gat ctc aaa tca atg gcg ctc  24238
Val Tyr Arg Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu
            1100                1105                1110

agt caa caa aat atg gat acg gaa ctt tcc act ctc tct tta tcc aat  24286
Ser Gln Gln Asn Met Asp Thr Glu Leu Ser Thr Leu Ser Leu Ser Asn
        1115                1120                1125

gag cta tta ttg gaa agc att aaa act gag tct aag ctg gat aat tat  24334
Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Asp Asn Tyr
    1130                1135                1140

act caa gtg atg gaa atg ctc tcc gct ttc cgt cct tcc ggc gcg acg  24382
Thr Gln Val Met Glu Met Leu Ser Ala Phe Arg Pro Ser Gly Ala Thr
1145                1150                1155                1160

cct tat cac gat gct tac gaa aat gtg cgt aaa gtt atc cag cta caa  24430
Pro Tyr His Asp Ala Tyr Glu Asn Val Arg Lys Val Ile Gln Leu Gln
                1165                1170                1175

gat cct ggg ctt gag caa tta aat gct tca cca gcc att gcc ggg ctg  24478
Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu
            1180                1185                1190

atg cat caa gct tcc cta tta ggt att aac gct tca atc tca cct gag  24526
Met His Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu
        1195                1200                1205

ttg ttt aat att ctg acg gag gag att act gaa ggt aat gct gag gaa  24574
Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu
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1210                1215                1220

ctt tat aag aaa aat ttt ggt aat atc gaa ccg gct tca ctg gct atg  24622
Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met
1225                1230                1235                1240

ccg gaa tac ctt aga cgt tat tac aat tta agt gat gaa gaa ctc agc  24670
Pro Glu Tyr Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser
                1245                1250                1255

cag ttt att ggt aaa gcc agc aat ttc ggc caa caa gaa tat agt aat  24718
Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn
            1260                1265                1270

aac caa ctc att act ccg ata gtc aac agc aat gat ggc acg gtc aag  24766
Asn Gln Leu Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys
        1275                1280                1285

gta tat cga att acc cgc gaa tat aca aca aat gcc aat caa gta gac  24814
Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr Asn Ala Asn Gln Val Asp
    1290                1295                1300

gtg gag ctg ttt ccc tac ggt ggg gaa aat tat cag tta aat tcc aaa  24862
Val Glu Leu Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys
1305                1310                1315                1320

ttc aaa gat tct cgt cag gat gtc tcc tat tta tcc atc aaa tta aat  24910
Phe Lys Asp Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn
                1325                1330                1335

gac aaa aga gaa ctt atc cga att gaa gga gtg cct cag gtc aac atc  24958
Asp Lys Arg Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile
            1340                1345                1350

gaa tat tca gaa cat atc acc tta agt aca act gat atc agt caa cct  25006
Glu Tyr Ser Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro
        1355                1360                1365

ttt gaa atc ggc cta aca cga gta tat cct tct agt tct tgg gca tat  25054
Phe Glu Ile Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr
    1370                1375                1380

gca gct gca aaa ttt acc att gag gaa tat aac caa tat tct ttc ctg  25102
Ala Ala Ala Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu
1385                1390                1395                1400

tta aaa cta aat aaa gct att cgt cta tct cgt gcg aca gaa tta tca  25150
Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser
                1405                1410                1415

ccc acc att ctg gaa agt att gtg cgt agt gtt aat cag gaa ctg gat  25198
Pro Thr Ile Leu Glu Ser Ile Val Arg Ser Val Asn Gln Glu Leu Asp
            1420                1425                1430

atc aac gca gaa gta tta ggt aaa gtt ttc ctg act aaa tat tat atg  25246
Ile Asn Ala Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met
        1435                1440                1445

caa cgt tat gct att aat gtt gaa act gcc cta ata cta tgc aat gca  25294
Gln Arg Tyr Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala
    1450                1455                1460

ctt att tca caa cgt tca tat gat aat caa cct agc caa ttt gat cgc  25342
Leu Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg
1465                1470                1475                1480
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ctg ttt aat acg cca tta ctg aac ggc caa tat ttt tct acc gga gat  25390
Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp
                1485                1490                1495

gaa gag att gat tta aat cca ggt agt act ggc gat tgg cgt aaa tcc  25438
Glu Glu Ile Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser
            1500                1505                1510

gtg ctt aaa cgt gca ttt aat atc gat gat att tcc ctc tac cgc ctg  25486
Val Leu Lys Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu
        1515                1520                1525

ctt aaa att acc aac cat aat caa gat gga aag att aaa aat aac      25534
Leu Lys Ile Thr Asn His Asn Gln Asp Gly Lys Ile Lys Asn Asn
    1530                1535                1540

tta aat aat ctt tct gat tta tat att ggg aaa tta ctg gca gaa att  25582
Leu Asn Asn Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile
1545                1550                1555                1560

cat caa tta acc att gat gaa ttg gat tta ttg ctg gtt gtc gtg ggt  25630
His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu Leu Val Ala Val Gly
                1565                1570                1575

gaa ggg gaa act aat tta tcc gct atc agt gat aaa caa ctg gcg gca  25678
Glu Gly Glu Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala
            1580                1585                1590

ctg atc aga aaa ctc aat acc att acc gtc tgg cta cag aca cag aag  25726
Leu Ile Arg Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys
        1595                1600                1605

tgg agt gcg ttc caa tta ttt gtt atg act tcc acc agc tat aac aaa  25774
Trp Ser Ala Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys
    1610                1615                1620

acg ctg acg cct gaa att aag aat ctg ctg gat aat gtc tac cac ggt  25822
Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly
1625                1630                1635                1640

tta caa ggc ttt gat aaa gac aag gca aat tta ctg cat gtt atg gcg  25870
Leu Gln Gly Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala
                1645                1650                1655

ccc tat att gcg gcc acc tta caa tta tca tcg gaa aat gtc gcc cat  25918
Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His
            1660                1665                1670

tct gtg ctg ctt tgg gca gac aag tta aag ccc ggc gac ggc gca atg  25966
Ser Val Leu Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met
        1675                1680                1685

acg gcc gaa aaa ttc tgg gac tgg ttg aat acc caa tat acg cca gat  26014
Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp
    1690                1695                1700

tca tcg gaa gta tta gcg acc cag gaa cat att gtt cag tat tgt cag  26062
Ser Ser Glu Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln
1705                1710                1715                1720

gcg ttg gcg caa tta gaa atg gtt tac cat tcc acc ggt att aat gaa  26110
Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu
                1725                1730                1735
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aac gcc ttc cgc ctg ttt gtg aca aaa cca gag atg ttt ggc tcg tca   26158
Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser
            1740                1745                1750

act gag gca gta cct gcg cat gat gca ctt tca ctg atc atg ctg acg   26206
Thr Glu Ala Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr
        1755                1760                1765

cgt ttt gca gat tgg gtt aat gcg tta ggc gaa aaa gcc tct tcc gta   26254
Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val
    1770                1775                1780

cta gcg gca ttt gaa gct aac agt tta acg gca gaa caa ttg gct gat   26302
Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp
1785                1790                1795                1800

gcc atg aat ctt gat gct aat ttg cta ttg caa gcc agt act caa gca   26350
Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala
                1805                1810                1815

caa aac cat caa cat ctt ccc cca gtg acg caa aaa aat gct ttc tcc   26398
Gln Asn His Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser
            1820                1825                1830

tgt tgg acg tct atc gac act atc ctg caa tgg gtt aat gtt gca caa   26446
Cys Trp Thr Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln
        1835                1840                1845

caa ttg aat gtc gcc cca cag gga gtt tcc gct ttg gtc ggg ctg gat   26494
Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp
    1850                1855                1860

tat att caa tta aat caa aaa atc ccc acc tat gcc cag tgg gaa agt   26542
Tyr Ile Gln Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser
1865                1870                1875                1880

gct ggg gaa ata ttg act gcc gga ttg aat tca caa cag gct gat ata   26590
Ala Gly Glu Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile
                1885                1890                1895

tta cac gct ttt ttg gac gaa tct cgc agt gcc gca tta agc act tac   26638
Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr
            1900                1905                1910

tat atc cgt caa gtc gcc aag cca ggg gca gcc ata aaa agc cgt gat   26686
Tyr Ile Arg Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp
        1915                1920                1925

gac ttg tac caa tat tta cta att gat aat cag gtt tcc gct gca atc   26734
Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile
    1930                1935                1940

aaa act acc cgg atc gcc gaa gcc att gcc agc att caa ctg tac gtc   26782
Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val
1945                1950                1955                1960

aac cgc agg ctg gaa aat gta gaa gaa aat gcc cat tca ggg gtt atc   26830
Asn Arg Thr Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile
                1965                1970                1975

agc cgt cag ttc ttt atc gac tgg gac aaa tat aac aaa cgc tac agc   26878
Ser Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser
            1980                1985                1990

acc tgg gcg ggt gtt tct caa tta gtt tac tac ccg gaa aac tat att   26926
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Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile
      1995                2000                2005

gat ccc acc atg cgt atc ggg caa acc aaa atg atg gac gca tta ttg   26974
Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu
   2010                2015                2020

caa tcc gtc agc caa agc caa tta aat gcc gat act gtc gaa gac gcc   27022
Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala
2025                2030                2035                2040

ttt atg tct tat ctg acc tcg ttt gag caa gtg gct aat ctt aaa gtt   27070
Phe Met Ser Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val
                2045                2050                2055

att agc ggg tat cac gat aat att aac aac ggt caa ggg ctg acc tat   27118
Ile Ser Ala Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr
            2060                2065                2070

ttt atc ggc ctc agt gaa act gat acc ggt gaa tac tat tgg cgc agt   27166
Phe Ile Gly Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser
        2075                2080                2085

gtc gat cac agt aaa ttc agc gac ggt aaa ttc gcc gct aat gcc tgg   27214
Val Asp His Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp
    2090                2095                2100

agt gaa tgg cac aaa att gat tgt cca att aat cct tac cga agc act   27262
Ser Glu Trp His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr
2105                2110                2115                2120

atc cgt cct gtg atg tac aaa tcc cgc ttg tat ctg ctc tgg ttg gaa   27310
Ile Arg Pro Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu
                2125                2130                2135

caa aag gag atc act aaa tca acc gga aat agc aaa gat ggc tat caa   27358
Gln Lys Glu Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln
            2140                2145                2150

acc gag aca gat tat cgt tat gag cta aaa ttg gcg cat atc cgt tat   27406
Thr Glu Thr Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr
        2155                2160                2165

gac ggt acc tgg aat acg cca atc act ttt gat gtc aat gaa aaa ata   27454
Asp Gly Thr Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile
    2170                2175                2180

tcc aag cta gaa ctg gca aaa aat aaa gcg cct ggg ctc tat tgt gct   27502
Ser Lys Leu Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala
2185                2190                2195                2200

ggt tat caa ggt gaa gat acg ttg ctg gtt atg ttt tat aac caa caa   27550
Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln
                2205                2210                2215

gat acc ctc gat agt tat aaa acc gct tca atg caa ggg cta tat atc   27598
Asp Thr Leu Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile
            2220                2225                2230

ttt gcc gat atg gaa tat aaa gat atg acc gat gga caa tac aaa tct   27646
Phe Ala Asp Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser
        2235                2240                2245

tac cgg gac aac agc tat aaa caa ttc gat act aat agt gtc aga aga   27694
Tyr Arg Asp Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg
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   2250                2255                2260

gtg aat aac cgc tat gca gag gat tat gaa att ccc tca tcg gta aat   27742
Val Asn Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn
2265                2270                2275                2280

agc cgt aaa ggc tat gat tgg gga gat tat tat ctc agt atg gta tat   27790
Ser Arg Lys Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr
                2285                2290                2295

aac gga gat att ccg acg att agt tat aaa gcc aca tca agt gat tta   27838
Asn Gly Asp Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu
            2300                2305                2310

aaa atc tat atc tcg cca aaa tta aga att att cat aat gga tat gaa   27886
Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu
        2315                2320                2325

ggg cag caa cgc aat caa tgc aat cta atg aat aaa tat ggc aaa cta   27934
Gly Gln Gln Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu
    2330                2335                2340

ggt gat aaa ttt att gtt tat act agc ttg gga gtt aat cca aat aat   27982
Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn
2345                2350                2355                2360

tcg tca aat aag ctg atg ttt tac ccc gtt tat caa tat aac gga aat   28030
Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn
                2365                2370                2375

gtc agt ggg ctt agt caa ggg aga tta cta ttc cac cgt gac acc aat   28078
Val Ser Gly Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn
            2380                2385                2390

tat tca tct aaa gta gaa gct tgg att cct gga gca gga cgt tct cta   28126
Tyr Ser Ser Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu
        2395                2400                2405

act aat cog aat gct gcc att ggt gat gat tat gct aca gac tcg tta   28174
Thr Asn Pro Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu
    2410                2415                2420

aac aaa ccg aat gat ctt aag caa tac gtc tat atg act gac agt aaa   28222
Asn Lys Pro Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys
2425                2430                2435                2440

ggt act gct acc gat gtc tca gga cca gta gat atc aat act gca att   28270
Gly Thr Ala Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile
                2445                2450                2455

tcc ccg gca aaa gtt cag gta acg gta aaa gcc ggt agc aaa gaa cag   28318
Ser Pro Ala Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln
            2460                2465                2470

agg ttt acc gcg gat aaa aat gtc tcc att cag cca tcc cct agc ttt   28366
Thr Phe Thr Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe
        2475                2480                2485

gat gaa atg aat tat caa ttt aat gct ctc gaa ata gat ggc tca agt   28414
Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser
    2490                2495                2500

ctg aat ttt act aac aat tca gcc agt act gat att acc ttt acc gca   28462
Leu Asn Phe Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala
2505                2510                2515                2520
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ttt gca gag gat gga cgt aaa ctg ggt tat gaa agt ttc agt att cct   28510
Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro
                2525                2530                2535

att acc cgc aag gtg agt act gat aat tat ctg acc ctg cgc cat aat   28558
Ile Thr Arg Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn
            2540                2545                2550

gaa aat ggt gcg caa tat atg caa tgg ggc gtc tat cgc att cgt ctt   28606
Glu Asn Gly Ala Gln Tyr Met Gln Trp Gly Val Tyr Arg Ile Arg Leu
        2555                2560                2565

aat act tta ttt gct cgc caa tta gtt gcg cga gcc act acc ggt att   28654
Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile
    2570                2575                2580

gat acg att ctg agt atg gaa act cag aat att cag gaa cca cag tta   28702
Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu
2585                2590                2595                2600

ggc aaa ggt ttc tac gct acg ttc gtg ata cct ccg tat aac cca tca   28750
Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser
                2605                2610                2615

act cat ggt gat gaa cgt tgg ttt aag ctt tat atc aaa cat gtc gtt   28798
Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val
            2620                2625                2630

gat aat aat tca cat att atc tat tca ggt cag cta aaa gat acg aat   28846
Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln Leu Lys Asp Thr Asn
        2635                2640                2645

ata agc acc acg tta ttt atc cct ctt gat gat gtt cca ttg aac caa   28894
Ile Ser Thr Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln
    2650                2655                2660

gat tac agt gct aag gtt tac atg acc ttc aag aaa tca tct tca gat   28942
Asp Tyr Ser Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp
2665                2670                2675                2680

ggt acc tgg tgg ggc cct cac ttt gtt aga gat gat aaa gga ata gta   28990
Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val
                2685                2690                2695

aca ata aac cct aaa tcc att ttg acc cac ttt gag agc gtc aat gtc   29038
Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val
            2700                2705                2710

ctg aat aat att agt agc gaa cca atg gat ttc agc ggc gct aac agc   29086
Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser
        2715                2720                2725

ctc tat ttt tgg gaa ctg ttc tac tat acc ccg atg ctg gtt gcc caa   29134
Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln
    2730                2735                2740

cgt ttg ttg cat gag caa aac ttt gat gaa gcg aac cgc tgg ctg aaa   29182
Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys
2745                2750                2755                2760

tat gtc tgg agc cca tcc ggg tat att gtt cac ggc cag att cag aat   29230
Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn
                2765                2770                2775
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tat caa tgg aac gtc cgc ccg tta ttg gaa gat acc agt tgg aac agt   29278
Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser
            2780                2785                2790

gat cct ttg gat tcc gtc gat cct gac gcg gta gcg cag cac gat ccg   29326
Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro
        2795                2800                2805

atg cac tat aaa gtt tca acc ttt atg cgc acc ctt gat ctg ttg atc   29374
Met His Tyr Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile
    2810                2815                2820

gcg cgc ggt gac cat gct tac cgt caa ttg gag cgc gat acg ctt aac   29422
Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn
2825                2830                2835                2840

gaa gcg aag atg tgg tat atg caa gcg ctg cat ctg tta ggt gat aaa   29470
Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys
                2845                2850                2855

cct tat ctg ccg ctg agt acc acg tgg aat gat cca cga ctg gac aaa   29518
Pro Tyr Leu Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys
            2860                2865                2870

gcc gcg gat att act acc caa agt gct cat tcc agt tca ata gtc gct   29566
Ala Ala Asp Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala
        2875                2880                2885

ttg cgg cag agt aca ccg gcg ctt tta tca ttg cgc agc gcc aat acc   29614
Leu Arg Gln Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr
    2890                2895                2900

ctg acc gat ctc ttc ctg ccg caa atc aat gaa gtg atg atg aat tac   29662
Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr
2905                2910                2915                2920

tgg caa acg tta gct cag aga gta tac aac ctg cgc cat aac ctc tct   29710
Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser
                2925                2930                2935

atc gac ggt cag ccg tta tat ctg cca atc tat gct aca ccg gcg gac   29758
Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp
            2940                2945                2950

ccg aaa gcg tta ctc agc gcc gct gtt gcc act tct caa ggt gga ggc   29806
Pro Lys Ala Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly
        2955                2960                2965

aag ctg ccg gag tca ttt atg tcc ctg tgg cgt ttc ccg cac atg ctg   29854
Lys Leu Pro Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu
    2970                2975                2980

gaa aat gct cgc agc atg gtt agc cag ctc acc caa ttc ggt tcc acg   29902
Glu Asn Ala Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr
2985                2990                2995                3000

tta caa aat att atc gaa cgt cag gac gca gta gcg ctc aat gcg tta   29950
Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala Val Ala Leu Asn Ala Leu
                3005                3010                3015

tta caa aat cag gcc gca gag ctg aaa ttg act aac ctg agt att caa   29998
Leu Gln Asn Gln Ala Ala Glu Leu Lys Leu Thr Asn Leu Ser Ile Gln
            3020                3025                3030

gac aac act ctt gaa gaa ctg gat gcc gag aaa acc gtg ctg gaa aaa   30046
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Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys
      3035                3040                3045

tcc aaa gcg gga gca caa tcg cgc ttt gat agc tat agc aaa ctg cat   30094
Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His
   3050                3055                3060

gat gaa aac atc aac gcc ggt gaa aac caa gct atg acg cta cga gcg   30142
Asp Glu Asn Ile Asn Ala Gly Glu Asn Gln Ala Met Thr Leu Arg Ala
3065                3070                3075                3080

tcc gca gcc ggg ctt acc acg gcg gtt cag gca tcc cgt ctg gcc ggc   30190
Ser Ala Ala Gly Leu Thr Thr Ala Val Gln Ala Ser Arg Leu Ala Gly
                3085                3090                3095

gca gcg gct gat ctg gtg cct aac atc ttc ggc ttc gcc ggt ggt ggt   30238
Ala Ala Ala Asp Leu Val Pro Asn Ile Phe Gly Phe Ala Gly Gly Gly
            3100                3105                3110

agc cgt tgg ggg gct atc gct gag gcg acc ggc tat gta atg gaa ttt   30286
Ser Arg Trp Gly Ala Ile Ala Glu Ala Thr Gly Tyr Val Met Glu Phe
        3115                3120                3125

tcc ggt aat gtt atg aat acc gaa gcg gat aaa att agc caa tct gaa   30334
Ser Ala Asn Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu
    3130                3135                3140

acc tac cgt cgt cgc cgt cag gag tgg gaa atc cag cgt aat aat gcc   30382
Thr Tyr Arg Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala
3145                3150                3155                3160

gaa gcg gag ctg aaa caa ctc gat gcc caa ctt aaa tcg ctg gca gtg   30430
Glu Ala Glu Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val
                3165                3170                3175

cgc cgt gaa gcc gcc gta ttg caa aaa acc agc ctg aaa acc caa caa   30478
Arg Arg Glu Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln
            3180                3185                3190

gag cag acc caa gcc caa ttg gcc ttc ctg caa cgt aag ttc agc aat   30526
Glu Gln Thr Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn
        3195                3200                3205

caa gcg ttg tac aac tgg cta cgt ggc cga ctg gca gca att tac ttc   30574
Gln Ala Leu Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Phe
    3210                3215                3220

cag ttc tac agc gac ttg gct atc gcg cgt tgt tta atg gca gag cag   30622
Gln Phe Tyr Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala
3225                3230                3235                3240

tac cgt tgg gaa atc agc gat gac tct gct cgc ttc atc aaa ccg ggc   30670
Tyr Arg Trp Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly
                3245                3250                3255

gcc tgg caa gga acc tat gca ggt ctg ctg gca cgt gaa acc ttg atg   30718
Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met
            3260                3265                3270

cta agt ttg gca caa atg gaa gac gcc cat tta aga cgt gat aaa cgc   30766
Leu Ser Leu Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg
        3275                3280                3285

gca tta gag gtc gaa cgt aca gta tcg ctg gcc gaa att tat gct ggt   30814
Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly
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  3290                3295                3300

tta ccg caa gat aaa ggc cca ttc tcc ctg acg caa gaa atc gag aag   30862
Leu Pro Gln Asp Lys Gly Pro Phe Ser Leu Thr Gln Glu Ile Glu Lys
3305                3310                3315                3320

ctg ggg aat gca ggt tca ggc agt ggc ggc agt ggt aat aat aat ttg   30910
Leu Val Asn Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu
                3325                3330                3335

gca ttt ggc gcc ggc acg gac act aaa act tct ttg cag gca tcc att   30958
Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile
            3340                3345                3350

tca tta gct gat tta aaa att cgt gag gat tac ccg gaa tct att ggc   31006
Ser Leu Ala Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly
        3355                3360                3365

aaa atc cgc cgc atc aaa cag atc agc gtt acc ctg cag gcg cta ttg   31054
Lys Ile Arg Arg Ile Lys Gln Ile Ser Val Thr Leu Gln Ala Leu Leu
    3370                3375                3380

ggc cct tac cag gat gtg cag gca ata tta tct tac ggc ggt aaa gcc   31102
Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Gly Lys Ala
3385                3390                3395                3400

gga tta gcg aac ggc tgt gca gcg ctg gcc gtt tcc cac ggt acg aat   31150
Gly Leu Ala Asn Gly Cys Ala Ala Leu Ala Val Ser His Gly Thr Asn
                3405                3410                3415

gac agc ggt caa ttc cag ctc gat ttc aac gat ggc aaa ttc ctg cag   31198
Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Phe Leu Gln
            3420                3425                3430

ttt gaa ggt att gcc att gat caa ggt acg cta aca ctg agt ttt cct   31246
Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro
        3435                3440                3445

aat gca tca acg cca gct aaa ggt aaa caa gcc act atg tta aaa acc   31294
Asn Ala Ser Thr Pro Ala Lys Gly Lys Gln Ala Thr Met Leu Lys Thr
    3450                3455                3460

ctg aac gat atc att ttg cat att cgc tac acc att aag taa           31336
Leu Asn Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Lys
3465                3470                3475

ccatccaac acagaactaa gccaggcccc gaatcggggt ctggtaaggg gtttct atg 31395
                                                              Met

cag aat tca cag aca ttc agt atg acc gag ctg tca tta cct aag ggc   31443
Gln Asn Ser Gln Thr Phe Ser Met Thr Glu Leu Ser Leu Pro Lys Gly
3480                3485                3490                3495

ggc ggc gcc att acc ggt atg ggt gaa gca tta acg ccg gcc ggg acg   31491
Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Ala Gly Pro
                3500                3505                3510

gat ggt atg gca gcc tta tcg ctg cca ttg ccc att tct gcc ggg cgt   31539
Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly Arg
            3515                3520                3525

ggt tat gcc ccc tcg ctc acg ctg aac tac aac agc gga acc ggt aac   31587
Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly Asn
        3530                3535                3540
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agc ccg ttc ggt ctc ggt tgg gac tgt aac gtc atg aca att cgt cgt   31635
Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg Arg
    3545                3550                3555

cgc acc agt acc ggc gtg ccg aat tat gat gaa acc gat act ttt ctg   31683
Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe Leu
3560                3565                3570                3575

ggg ccg gaa ggt gaa gtg ttg gtc gta gcg tta aat gag gca ggt caa   31731
Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly Gln
                3580                3585                3590

gct gat atc cgc agt gaa tcc tca tta cag ggc atc aat ttg ggg atg   31779
Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly Met
            3595                3600                3605

acc ttc acc gtt acc ggt tat cgc tcc cgt ttg gaa agc cac ttt agc   31827
Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe Ser
        3610                3615                3620

cgg ttg gaa tac tgg caa ccc cag aca acg ggc gca acc gat ttc tgg   31875
Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe Trp
    3625                3630                3635

ctg ata tac agc ccc gac gga caa gcc cat tta ctg ggc aaa aat cct   31923
Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn Pro
3640                3645                3650                3655

caa gca cgc atc agc aat ccg cta aat gtt acc caa aca gcg caa tgg   31971
Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln Trp
                3660                3665                3670

ctg ttg gaa gcc tcg gta tca tcc cac ggc gag cag att tat tat cag   32019
Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr Gln
            3675                3680                3685

tat cga gcc gaa gat gaa act gat tgc gaa act gac gaa ctc aca gcc   32067
Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr Ala
        3690                3695                3700

cac ccg aac aca acc gtc cag cgc tac ttg caa gta gta cat tac ggt   32115
His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr Gly
    3705                3710                3715

aat cta acc gcc agc gaa gta ttt ccc acg cta aat ggg gat gat cca   32163
Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp Pro
3720                3725                3730                3735

ctc aaa tct ggc tgg ttg ttc ttg tta gta ttt gat tac ggt gag cgc   32211
Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu Arg
                3740                3745                3750

aaa aac agc tta tct gaa atg ccg cca ttt aaa gcc aca agt aac tgg   32259
Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn Trp
            3755                3760                3765

ctt tgc cgc aaa gac cgt ttt tcc cgt tat gaa tac ggt ttt gca ttg   32307
Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala Leu
        3770                3775                3780

cgc acc cgg cgc tta tgt cgc caa ata ctg atg ttt cac cgt ctg caa   32355
Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu Gln
    3785                3790                3795

acc ctg tct ggt cag gca aaa ggc gac gat gaa ccc gca tta gtt tca   32403
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Thr Leu Ser Gly Gln Ala Lys Gly Asp Asp Glu Pro Ala Leu Val Ser
3800                3805                3810                3815

cgt ctg ata ctg gat tat gac gaa aac gcg gtg gtc agt acg ctc gtt   32451
Arg Leu Ile Leu Asp Tyr Asp Glu Asn Ala Val Val Ser Thr Leu Val
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tct gtc cgc cga gtg gga cat gag caa gat ggc aca acg gcg gtc gcc   32499
Ser Val Arg Arg Val Gly His Glu Gln Asp Gly Thr Thr Ala Val Ala
            3835                3840                3845

ctg ccg cca ttg gaa ctg gct tat cag cct ttt gaa cca gaa caa aaa   32547
Leu Pro Pro Leu Glu Leu Ala Tyr Gln Pro Phe Glu Pro Glu Gln Lys
        3850                3855                3860

gca ctc tgg cga cca atg gat gta ctg gcg aat ttc aac acc atc caa   32595
Ala Leu Trp Arg Pro Met Asp Val Leu Ala Asn Phe Asn Thr Ile Gln
    3865                3870                3875

cgc tgg caa ctg ctt gat ctg caa ggc gaa ggc gta ccc ggt att ctg   32643
Arg Trp Gln Leu Leu Asp Leu Gln Gly Glu Gly Val Pro Gly Ile Leu
3880                3885                3890                3895

tat cag gat aaa aat ggc tgg tgg tat cgc tct gct caa cgt cag acc   32691
Tyr Gln Asp Lys Asn Gly Trp Trp Tyr Arg Ser Ala Gln Arg Gln Thr
                3900                3905                3910

ggg gaa gag atg aat gcg gtc acc tgg ggc aaa atg caa ctc ctt cct   32739
Gly Glu Glu Met Asn Ala Val Thr Trp Gly Lys Met Gln Leu Leu Pro
            3915                3920                3925

atc acg ccc gct att cag gat aac gcc tca ctg atg gat att aat ggt   32787
Ile Thr Pro Ala Ile Gln Asp Asn Ala Ser Leu Met Asp Ile Asn Gly
        3930                3935                3940

gat ggg caa ctg gat tgg gtt atc acc ggt ccg ggg cta agg ggt tat   32835
Asp Gly Gln Leu Asp Trp Val Ile Thr Gly Pro Gly Leu Arg Gly Tyr
    3945                3950                3955

cac agc cag cat cca gat ggc agt tgg acg cgt ttt agg ccg ttg ccc   32883
His Ser Gln His Pro Asp Gly Ser Trp Thr Arg Phe Thr Pro Leu His
3960                3965                3970                3975

gcc tta ccg ata gaa tat acc cat ccc cgc gcc caa ctt gcg gat tta   32931
Ala Leu Pro Ile Glu Tyr Thr His Pro Arg Ala Gln Leu Ala Asp Leu
                3980                3985                3990

atg ggg gcc ggg ctg tcc gat tta gtg ctg att ggt ccc aaa agc gtg   32979
Met Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro Lys Ser Val
            3995                4000                4005

cgt ttg tat gcc aat aac cgt gat ggt ttt acc gaa gga cgg gat gtg   33027
Arg Leu Tyr Ala Asn Asn Arg Asp Gly Phe Thr Glu Gly Arg Asp Val
        4010                4015                4020

gtg caa tcc ggt ggt atc acc ctg ccg tta ccg ggc gcc gat gcg cgt   33075
Val Gln Ser Gly Gly Ile Thr Leu Pro Leu Pro Gly Ala Asp Ala Arg
    4025                4030                4035

aag tta gtg gcc ttt agc gac gta ctc ggt tca ggc caa gca cat ttg   33123
Lys Leu Val Ala Phe Ser Asp Val Leu Gly Ser Gly Gln Ala His Leu
4040                4045                4050                4055

gtt gaa gtt agt gcg acg aaa gtc acc tgc tgg cca aat ctg gga cat   33171
Val Glu Val Ser Ala Thr Lys Val Thr Cys Trp Pro Asn Leu Gly His
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ggc cgt ttt ggt cag cca atc acc ttg ccg gga ttt agc caa tcc gcc   33219
Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser Ala
            4075                4080                4085

gcc aat ttt aat cct gat cga gtt cat ctg gcc gat ctg gac ggt agt   33267
Ala Asn Phe Asn Pro Asp Arg Val Ile Leu Ala Asp Leu Asp Gly Ser
        4090                4095                4100

ggt cct gcc gat ctg att tat gtt cat gct gac cac ctg gat att ttc   33315
Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile Phe
    4105                4110                4115

agc aat gaa agt ggc aac ggt ttt gca caa cca ttc aca ctc cgt ttt   33363
Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg Phe
4120                4125                4130                4135

cct gac ggc ctg cgt ttt gat gat act tgc cag cta caa gtg gct gat   33411
Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala Asp
                4140                4145                4150

gta cag ggg tta ggg gtt gtc agc ctg atc ctg agc gta ccg cat atg   33459
Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His Met
            4155                4160                4165

gcg cca cac cat tgg cgc tgc gat ctg acc aac gcg aaa ccg tgg tta   33507
Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp Leu
        4170                4175                4180

ctc agt gaa atg aac aac aac atg ggc gcc cat cac acc ctg cat tac   33555
Leu Ser Glu Met Asn Asn Asn Met Gly Ala His His Thr Leu His Tyr
    4185                4190                4195

cgt agc tcc gtc cag ttt tgg ctg gat gaa aaa gcc gca gcc tta gct   33603
Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu Ala
4200                4205                4210                4215

acc gga caa aca ccg gtc tgt tac ctg ccc ttc ccg gtc cat acc ctg   33651
Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr Leu
                4220                4225                4230

tgg caa aca gaa acc gag gat gaa atc agc ggc aat aaa tta gtg acc   33699
Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val Thr
            4235                4240                4245

act tta cgt tac gct cac ggc gcc tgg gat gga cgt gag cgg gaa ttt   33747
Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu Phe
        4250                4255                4260

cgc ggc ttt ggc tat gtt gag cag acg gac agc cat caa ctg gct caa   33795
Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Gln Leu Ala Gln
    4265                4270                4275

ggc aat gcg ccg gaa cgt aca tca ccg gca ctt acc aaa aac tgg tat   33843
Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp Tyr
4280                4285                4290                4295

gcc acc gga atc cct gag gta gac aat acg cta tct gcc ggg tat tgg   33891
Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr Trp
                4300                4305                4310

cgc ggt gat acg cag gct ttc act ggt ttt acg cca cac ttt act ctc   33939
Arg Gly Asp Thr Gln Ala Phe Thr Gly Phe Thr Pro His Phe Thr Leu
            4315                4320                4325
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tgg aaa gag ggc aaa gat gtt cca ctg aca ccg gaa gat gac cac aat   33987
Trp Lys Glu Gly Lys Asp Val Pro Leu Thr Pro Glu Asp Asp His Asn
        4330                4335                4340

ctg tac tgg tta aac cgg gca cta aaa ggt caa cca ctg cgt agt gaa   34035
Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser Glu
    4345                4350                4355

ctc tac ggg cta gat ggc agc gca cag cag aag atc ccc tat aca gtg   34083
Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr Val
4360                4365                4370                4375

act gaa tcc cgc cca caa gtg cgc caa tta caa gat aac act acc ctt   34131
Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr Leu
                4380                4385                4390

tcc ccg gtg ctc tgg gcc tca gtg gtg gaa agt cgt agt tat cac tat   34179
Ser Pro Val Leu Trp Ala Ser Val Val Glu Ser Arg Ser Tyr His Tyr
            4395                4400                4405

gaa cgt atc atc agc gat ccc caa tgc aat cag gat atc act ctg tcc   34227
Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu Ser
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agt gac cta ttc ggg caa ccg ctg aaa cag gtt tca gtg caa tat ccc   34275
Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr Pro
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cgc cgc aat aaa cca aca acc aat ccg tat ccc gat aca cta cca gat   34323
Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro Asp
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act ctg ttt gcc agc agt tat gac gac caa caa cta ttg cgg tta   34371
Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg Leu
                4460                4465                4470

acc tac cag caa tcc agt tgg cat cat cta att gct aat gaa ctc aga   34419
Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu Arg
            4475                4480                4485

gtg tta gga tta ccg gat ggt aca cgc agt gat gct ttc act tac gat   34467
Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr Asp
        4490                4495                4500

gct aaa cac gtg cct gtt gat ggt tta aat ctg gaa gct cta tgt gct   34515
Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys Ala
    4505                4510                4515

gaa aat agc ctg att gcc gat gat aaa act cgc gaa tac ctc aac cag   34563
Glu Asn Ser Leu Ile Ala Asp Asp Lys Thr Arg Glu Tyr Leu Asn Gln
4520                4525                4530                4535

caa cga acg ttc tat acc gat ggg aaa acc gat gga aac aat cca acg   34611
Gln Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro Thr
                4540                4545                4550

cca ctg aaa aca ccg aca cga cag gct tta atc gcc ttt acc gaa acg   34659
Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu Thr
            4555                4560                4565

gcg gta tta acg gaa tct ctg tta tcc gca ttt gat ggc ggc atc acg   34707
Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Phe Asp Gly Gly Ile Thr
        4570                4575                4580
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cca gat gaa tta ccc ggc ctt ctg cca caa gca gga tac caa caa gaa   34755
Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln Glu
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cct tat ctg ttc cca ctc agt ggc gaa aac caa gtc tgg gta gca cgc   34803
Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala Arg
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aaa ggc tat acc gat tac gga act gag gta caa ttt tgg cgt cct gtc   34851
Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro Val
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gca caa cgt aac acc cag tta acc ggg aaa acg act cta aaa tgg gat   34899
Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp Asp
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acc cac tac tgt gtc atc act caa acc caa gac gcg gct ggt ttg act   34947
Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu Thr
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gtc tca gcc aat tat gac tgg cgt ttt ctc aca cct atg caa ctg act   34995
Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu Thr
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gat atc aac gat aat gtg cat atc ata acc ttg gat gcg cta ggg cgc   35043
Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly Arg
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cct gtc act caa cgt ttc tgg gga atc gaa aat ggt gtg gca aca ggt   35091
Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr Gly
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tac tct tca cca gaa gca aaa cca ttc act cca cca gtc gat gtc aat   35139
Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val Asn
            4715                4720                4725

gct gcc att gct ctg acc gga cca ctc cct gtc gcg cag tgt ctg gtc   35187
Ala Ala Ile Ala Leu Thr Gly Pro Leu Pro Val Ala Gln Cys Leu Val
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tat gcg ccg gac agt tgg atg ccg ctt ttc ggt cag gaa acc ttc aac   35235
Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe Asn
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aca tta acg ccg gaa gag caa aag acc ctg cgt gat tta cgg att atc   35283
Thr Leu Thr Gln Glu Glu Gln Lys Thr Leu Arg Asp Leu Arg Ile Ile
4760                4765                4770                4775

acc gaa gat tgg cgt att tgc gca ctg gct cgc cgc cgt tgg cta caa   35331
Thr Glu Asp Trp Arg Ile Cys Ala Leu Ala Arg Arg Arg Trp Leu Gln
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agt caa aaa gcc ggc acg cca ttg gtt aag ctg tta acc aac agc atc   35379
Ser Gln Lys Ala Gly Thr Pro Leu Val Lys Leu Leu Thr Asn Ser Ile
            4795                4800                4805

ggt tta cct ccc cac aac ctc atg ctg gct acg gac cgt tat gac cgt   35427
Gly Leu Pro Pro His Asn Leu Met Leu Ala Thr Asp Arg Tyr Asp Arg
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gat tct gaa cag caa att cgt caa caa gtc gca ttc agt gat ggt ttt   35475
Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly Phe
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Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala Trp
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caa cgt aac caa gac ggt tct ctg gtg acc aaa atg gaa gat acc aaa   35571
Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr Lys
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acg cgc tgg gcg att acg gga cgc act gaa tat gac aat aag ggg cag   35619
Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly Gln
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gcg ata cga act tat cag ccc tat ttg ctc aat gac tgg cga tat gtg   35667
Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr Val
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agt gat gac agc gcc gcc agg aaa gag gcc tat gcc gat act cat atc tat   35715
Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile Tyr
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gat ccg att ggg cgg gaa atc caa gtt atc acg gca aaa gtc tgg ctg   35763
Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp Leu
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Arg Gln Asn Gln Tyr Phe Pro Trp Phe Thr Val Ser Glu Asp Glu Asn
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Ile Leu Cys Thr Glu Ser Val Asp Ala Gly Arg Thr Val Thr Leu Asn
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Asp Ile Glu Gly Arg Pro Leu Leu Thr Val Thr Ala Thr Gly Val Ile
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Leu Thr Tyr Asp Val Ala Gly Glu Leu Asn Gly Ser Trp Leu Thr Leu
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Pro Val Gly Asn Val Ile Ser Ile Arg Asn Asp Ala Glu Ala Thr Arg
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Phe Trp His Asn Gln Lys Val Ala Pro Glu Asn Thr Tyr Thr Tyr Asp
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Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu Met Ala Asn Ile
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Gly Gln Gln Ser Asn Gln Leu Pro Ser Leu Thr Leu Pro Ser Asp Asn
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Arg Met Val Arg Asn Asn Pro Val Thr Leu Leu Asp Pro Asp Gly Leu
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Met Pro Thr Ile Ala Glu Arg Ile Ala Ala Leu Gln Lys Asn Lys Val
675 680 685

Ala Asp Ser Ala Pro Ser Pro Thr Asn Ala Thr Asn Val Ala Ile Asn
690 695 700

Ile Arg Pro Pro Val Ala Pro Lys Pro Thr Leu Pro Lys Ala Ser Thr
705 710 715 720

Ser Ser Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro
725 730 735

Thr Thr Ser Gly Ser Ser Ile Thr Ala Pro Leu Ser Pro Val Gly Asn
740 745 750

Lys Ser Thr Pro Glu Ile Ser Leu Pro Glu Ser Thr Gln Ser Asn Ser
755 760 765

Ser Ser Ala Ile Ser Thr Asn Leu Gln Lys Lys Ser Phe Thr Leu Tyr
770 775 780

Arg Ala Asp Asn Arg Ser Phe Glu Asp Met Gln Ser Lys Phe Pro Glu
785 790 795 800

Gly Phe Lys Ala Trp Thr Pro Leu Asp Thr Lys Met Ala Arg Gln Phe
805 810 815

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Ala Ser Val Phe Ile Gly Gln Lys Asp Thr Ser Asn Leu Pro Lys Glu
            820                 825                 830

Thr Val Lys Asn Ile Asn Thr Trp Gly Thr Lys Pro Lys Leu Asn Asp
        835                 840                 845

Leu Ser Thr Tyr Ile Lys Tyr Thr Lys Asp Lys Ser Thr Val Trp Val
    850                 855                 860

Ser Thr Ala Ile Asn Thr Glu Ala Gly Gly Gln Ser Ser Gly Ala Pro
865                 870                 875                 880

Leu His Glu Ile Asn Met Asp Leu Tyr Glu Phe Thr Ile Asp Gly Gln
                885                 890                 895

Lys Leu Asn Pro Leu Pro Arg Gly Arg Ser Lys Asp Arg Val Pro Ser
            900                 905                 910

Leu Leu Leu Asp Thr Pro Glu Ile Glu Thr Ala Ser Ile Ile Ala Leu
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Pro Leu Lys Asn Val Lys Pro Tyr Lys Arg
945                 950


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            20                  25                  30

His Ser Ser Phe Asn Glu Phe His Gln Gln Val Ser Glu His Leu Ser
        35                  40                  45

Trp Ser Glu Ala His Asp Leu Tyr His Asp Ala Gln Gln Ala Gln Lys
    50                  55                  60

Asp Asn Arg Leu Tyr Glu Ala Arg Ile Leu Lys Arg Thr Asn Pro Gln
65                  70                  75                  80

Leu Gln Asn Ala Val His Leu Ala Ile Val Ala Pro Asn Ala Glu Leu
                85                  90                  95

Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val Ala
            100                 105                 110

Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr Glu
        115                 120                 125

Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr Arg
    130                 135                 140

Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln Gln
145                 150                 155                 160
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Asn Met Asp Thr Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu Leu
165 170 175

Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Asp Asn Tyr Thr Gln Val
180 185 190

Met Glu Met Leu Ser Ala Phe Arg Pro Ser Gly Ala Thr Pro Tyr His
195 200 205

Asp Ala Tyr Glu Asn Val Arg Lys Val Ile Gln Leu Gln Asp Pro Gly
210 215 220

Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His Gln
225 230 235 240

Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe Asn
245 250 255

Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr Lys
260 265 270

Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu Tyr
275 280 285

Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe Ile
290 295 300

Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln Leu
305 310 315 320

Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys Val Tyr Arg
325 330 335

Ile Thr Arg Glu Tyr Thr Thr Asn Ala Asn Gln Val Asp Val Glu Leu
340 345 350

Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys Phe Lys Asp
355 360 365

Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg
370 375 380

Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser
385 390 395 400

Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro Phe Glu Ile
405 410 415

Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr Ala Ala Ala
420 425 430

Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu
435 440 445

Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile
450 455 460

Leu Glu Ser Ile Val Arg Ser Val Asn Gln Gln Leu Asp Ile Asn Ala
465 470 475 480

Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr
485 490 495

Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Leu Ile Ser
500 505 510

Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn
515 520 525

Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile
530 535 540

Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser Val Leu Lys
545 550 555 560

Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu Leu Lys Ile
565 570 575

Thr Asn His Asn Asn Gln Asp Gly Lys Ile Lys Asn Asn Leu Asn Asn
580 585 590

Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile His Gln Leu
595 600 605

Thr Ile Asp Glu Leu Asp Leu Leu Leu Val Ala Val Gly Glu Gly Glu
610 615 620

Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala Leu Ile Arg
625 630 635 640

Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys Trp Ser Ala
645 650 655

Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
660 665 670

Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
675 680 685

Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala Pro Tyr Ile
690 695 700

Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu
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Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met Thr Ala Glu
725 730 735

Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp Ser Ser Glu
740 745 750

Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala
755 760 765

Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe
770 775 780

Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser Thr Glu Ala
785 790 795 800

Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala
805 810 815

Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala
820 825 830

Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn
835 840 845

Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala Gln Asn His

850 855 860

Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser Cys Trp Thr
865 870 875 880

Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Asn
885 890 895

Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp Tyr Ile Gln
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Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser Ala Gly Glu
915 920 925

Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile Leu His Ala
930 935 940

Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg
945 950 955 960

Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr
965 970 975

Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr
980 985 990

Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Thr
995 1000 1005

Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile Ser Arg Gln
1010 1015 1020

Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala
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Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr
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Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val
1060 1065 1070

Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Pro Met Ser
1075 1080 1085

Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala
1090 1095 1100

Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly
1105 1110 1115 1120

Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser Val Asp His
1125 1130 1135

Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
1140 1145 1150

His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr Ile Arg Pro
1155 1160 1165

Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
1170 1175 1180

Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
1185 1190 1195 1200

Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
1205 1210 1215

Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile Ser Lys Leu
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Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
1235 1240 1245

Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
1250 1255 1260

Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
1265 1270 1275 1280

Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser Tyr Arg Asp
1285 1290 1295

Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg Val Asn Asn
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Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn Ser Arg Lys
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Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
1330 1335 1340

Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu Lys Ile Tyr
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Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Gln
1365 1370 1375

Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
1380 1385 1390

Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
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Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn Val Ser Gly
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Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn Tyr Ser Ser
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Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu Thr Asn Pro
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Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro
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Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys Gly Thr Ala
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Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile Ser Pro Ala
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Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln Thr Phe Thr
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Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met
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Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser Leu Asn Phe
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Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala Phe Ala Glu
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Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Ile Thr Arg
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Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn Glu Asn Gly
1585 1590 1595 1600

Ala Gln Tyr Met Glu Trp Gly Val Tyr Arg Ile Arg Leu Asn Thr Leu
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Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile
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Leu Ser Met Glu Thr Gln Asn Ile Glu Glu Pro Gln Leu Gly Lys Gly
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Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser Thr His Gly
1650 1655 1660

Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn
1665 1670 1675 1680

Ser His Ile Ile Tyr Ser Gly Glu Leu Lys Asp Thr Asn Ile Ser Thr
1685 1690 1695

Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr Ser
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Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp
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Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn
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Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn
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Thr Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe
1765 1770 1775

Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu
1780 1785 1790

His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp
1795 1800 1805

Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp
1810 1815 1820

Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu
1825 1830 1835 1840

Asp Ser Val Asp Pro Asp Ala Val Ala Glu His Asp Pro Met His Tyr
1845 1850 1855

Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly
1860 1865 1870

Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys
1875 1880 1885

Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu

1890 1895 1900

Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys Ala Ala Asp
905 1910 1915 1920

Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala Leu Arg Gln
1925 1930 1935

Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr Leu Thr Asp
1940 1945 1950

Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr Trp Gln Thr
1955 1960 1965

Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser Ile Asp Gly
1970 1975 1980

Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp Pro Lys Ala
985 1990 1995 2000

Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly Lys Leu Pro
2005 2010 2015

Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu Glu Asn Ala
2020 2025 2030

Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr Leu Gln Asn
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Ile Ile Glu Arg Gln Asp Ala Glu Ala Leu Asn Ala Leu Leu Gln Asn
2050 2055 2060

Gln Ala Ala Glu Leu Ile Leu Thr Asn Leu Ser Ile Gln Asp Lys Thr
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Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys Ser Lys Ala
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Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His Asp Glu Asn
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Asp Leu Val Pro Asp Ile Phe Gly Phe Ala Gly Gly Gly Ser Arg Trp
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Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu Thr Tyr Arg
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Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala Glu Ala Glu
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Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val Arg Arg Glu
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Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln Glu Gln Thr
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Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn Gln Ala Leu
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Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Ile Gln Phe Tyr
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Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp
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Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln
2290 2295 2300

Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met Leu Ser Leu
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Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg Ala Leu Glu
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Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly Leu Pro Gln
2340 2345 2350

Asp Lys Gly Pro Phe Ser Leu Thr Gln Glu Ile Glu Lys Leu Val Asn
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Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly
2370 2375 2380

Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile Ser Leu Ala
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Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly Lys Ile Arg
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Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr
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Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala
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2450 2455 2460

Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Pro Leu Pro Phe Glu Gly
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Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser
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Arg Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly
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Asn Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg
65 70 75 80

Arg Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe
85 90 95

Leu Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly
100 105 110

Gln Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly
115 120 125

Met Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe
130 135 140

Ser Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe
145 150 155 160

Trp Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn
165 170 175

Pro Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln
180 185 190

Trp Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr
195 200 205

Gln Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr
210 215 220

Ala His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr
225 230 235 240

Gly Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp
245 250 255

Pro Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu
260 265 270

Arg Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn
275 280 285

Trp Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala
290 295 300

Leu Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu
305 310 315 320

Gln Thr Leu Ser Gly Gln Ala Lys Gly Asp Asp Glu Pro Ala Leu Val
325 330 335

Ser Arg Leu Ile Leu Asp Tyr Asp Glu Asn Ala Val Val Ser Thr Leu
340 345 350

Val Ser Val Arg Arg Val Gly His Glu Gln Asp Gly Thr Thr Ala Val
355 360 365

Ala Leu Pro Pro Leu Glu Leu Ala Tyr Gln Pro Phe Glu Pro Glu Gln
370 375 380

Lys Ala Leu Trp Arg Pro Met Asp Val Leu Ala Asn Phe Asn Thr Ile
385 390 395 400

Gln Arg Trp Gln Leu Leu Asp Leu Gln Gly Glu Gly Val Pro Gly Ile
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Leu Tyr Gln Asp Lys Asn Gly Trp Trp Tyr Arg Ser Ala Gln Arg Gln
420 425 430

Thr Gly Glu Glu Met Asn Ala Val Thr Trp Gly Lys Met Gln Leu Leu
435 440 445

Pro Ile Thr Pro Ala Ile Gln Asp Asn Ala Ser Leu Met Asp Ile Asn
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Gly Asp Gly Gln Leu Asp Trp Val Ile Thr Gly Pro Gly Leu Arg Gly
465 470 475 480

Tyr His Ser Gln His Pro Asp Gly Ser Trp Thr Arg Phe Thr Pro Leu
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His Ala Leu Pro Ile Glu Tyr Thr His Pro Arg Ala Gln Leu Ala Asp
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Leu Met Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro Lys Ser
515 520 525

Val Arg Leu Tyr Ala Asn Asn Arg Asp Gly Phe Thr Glu Gly Arg Asp
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Val Val Gln Ser Gly Gly Ile Thr Leu Pro Leu Pro Gly Ala Asp Ala
545 550 555 560

Arg Lys Leu Val Ala Phe Ser Asp Val Leu Gly Ser Gly Gln Ala His
565 570 575

Leu Val Glu Val Ser Ala Thr Lys Val Thr Cys Trp Pro Asn Leu Gly
580 585 590

His Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser
595 600 605

Ala Ala Asn Phe Asn Pro Asp Arg Val His Leu Ala Asp Leu Asp Gly
610 615 620

Ser Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile
625 630 635 640

Phe Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg
645 650 655

Phe Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala
660 665 670

Asp Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His
675 680 685

Met Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp
690 695 700

Leu Leu Ser Glu Met Asn Asn Asn Met Gly Ala His His Thr Leu His
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Tyr Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu
725 730 735

Ala Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr
740 745 750

Leu Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val
755 760 765

Thr Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu
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Phe Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Glu Leu Ala
785 790 795 800

Gln Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp
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Tyr Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr
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Asn Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser
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Glu Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr
885 890 895

Val Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr
900 905 910

Leu Ser Pro Val Leu Trp Ala Ser Val Val Glu Ser Arg Ser Tyr His
915 920 925

Tyr Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu
930 935 940

Ser Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr
945 950 955 960

Pro Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro
965 970 975

Asp Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg
980 985 990

Leu Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu
995 1000 1005

Arg Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr
1010 1015 1020

Asp Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys
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Ala Glu Asn Ser Leu Ile Ala Asp Asp Lys Pro Arg Glu Tyr Leu Asn
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Gln Glu Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro

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Thr Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu
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Thr Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Thr Asp Gly Gly Ile
1090 1095 1100

Thr Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln
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Glu Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala
1125 1130 1135

Arg Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro
1140 1145 1150

Val Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp
1155 1160 1165

Asp Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu
1170 1175 1180

Thr Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu
185 1190 1195 1200

Thr Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly
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Arg Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr
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Gly Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val
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Asn Ala Ala Ile Ala Leu Thr Gly Pro Leu Pro Val Ala Gln Cys Leu
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Val Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe
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Asn Thr Leu Thr Gln Glu Glu Gln Lys Thr Leu Arg Asp Leu Arg Ile
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Ile Thr Glu Asp Trp Arg Ile Cys Ala Leu Ala Arg Arg Arg Trp Leu
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Gln Ser Gln Lys Ala Gly Thr Pro Leu Val Lys Leu Leu Thr Asn Ser
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Ile Gly Leu Pro Pro His Asn Leu Met Leu Ala Thr Asp Arg Tyr Asp
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Arg Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly
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Phe Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala
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Trp Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr
1380 1385 1390

Lys Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly
1395 1400 1405

Gln Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr
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Val Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile
1425 1430 1435 1440

Tyr Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp
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Leu Arg Gln Asn Gln Tyr Phe Pro Trp Phe Thr Val Ser Glu Asp Glu
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Asn Asp Leu Ser Ala Asp Ala Leu Val
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(54) Title: INSECTICIDAL TOXINS FROM PHOTORHABDUS

(57) Abstract

Novel nucleic acid sequences isolated from *Photorhabdus luminescens*, whose expression results in novel insecticidal toxins, are disclosed herein. The invention also discloses compositions and formulations containing the insecticidal toxins that are capable of controlling insect pests. The invention is further drawn to methods of making the toxins and to methods of using the nucleotide sequences, for example in microorganisms to control insect pests or in transgenic plants to confer insect resistance.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 01015

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/31 C12N15/82 C12N15/10 C12N1/21 C12N5/10
A01H5/00 C07K14/24 A01N63/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N A01H C07K A01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 17432 A (WISCONSIN ALUMNI RES FOUND) 15 May 1997 (1997-05-15) the whole document, particularly SEQ ID NOS 31,46,47,48,49,50,51,60 ---	1-3,7-9, 11-24, 26-36
P,X	WO 98 08932 A (DOW AGROSCIENCES LLC ;WISCONSIN ALUMNI RES FOUND (US)) 5 March 1998 (1998-03-05) see pages 209-210,215-224,231-237, and 243-245. --- -/--	1-3,7-9, 11-24, 26-36

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
20 October 1999	08. 11. 99

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Maddox, A

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DAVID JOSEPH BOWEN: "Characterization of a High Molecular Weight Insecticidal Protein Complex Produced by the Entomopathogenic Bacterium Photorhabdus luminescens (Nematodes, Biological Control)" THESIS UNIVERSITY WISCONSIN, 1 May 1995 (1995-05-01), XP002076022 see chapter 3 ---	1-36
A	WO 95 00647 A (COMMW SCIENT IND RES ORG ;SMIGIELSKI ADAM JOSEPH (AU); AKHURST RAY) 5 January 1995 (1995-01-05) the whole document ---	1-36
A	SZITTNER, R., ET AL.: "Nucleotide sequence, expression, and properties of luciferase coded by the lux genes from a terrestrial bacterium" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 265, no. 27, 1990, pages 16581-16587, XP002119674 figure 5 ---	2,11
A	WO 93 07278 A (CIBA GEIGY AG) 15 April 1993 (1993-04-15) the whole document ---	12-19, 29-34
P,A	WO 98 08388 A (MORGAN JAMES ALUN WYNNE ;JARRETT PAUL (GB); ELLIS DEBORAH JUNE (GB) 5 March 1998 (1998-03-05) see SEQ ID NO:1 -----	1-36

INTERNATIONAL SEARCH REPORT

...ernati... application No.
PCT/EP 99/ 01015

Box I Obs rvations wher certain claims were found unsearchable (Continuation f item 1 of first sh et)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☒ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

B x II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 4,5,6,10,25 all completely, and 1-3,12-24, 27-36 all partially

Nucleic acid molecule comprising the claimed regions of sequence ID 1, chimeric genes and hosts containing said molecule, toxins expressed by said regions,and method for producing said toxins and controlling insects using said toxins, method for mutagenizing said nucleic acid molecules.

2. Claims: 7-9,11,26 all completely, and 1-3,12-24, 27-36 all partially

Nucleic acid molecule comprising the claimed regions of sequence ID 11, chimeric genes and hosts containing said molecule, toxins expressed by said regions,and method for producing said toxins and controlling insects using said toxins, method for mutagenizing said nucleic acid molecules.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box 3.

The reference to claim 44 in claim 30 is inconsistent with the numbering of the claims, since claim 44 has not been filed. For the purpose of defining the search, claim 30 has been considered to refer to the toxin of claim 20, and searched accordingly.

INTERNATIONAL SEARCH REPORT

Intr tional Application No
PCT/EP 99/01015

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